

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 09:26:01 ; Search time 19.743 seconds
(without alignments)
4694.096 Million cell updates/sec

Title: US-10-045-631B-88_COPY_2_329

Perfect score: 1686

Sequence: 1 AEEGAVAVCVVRPLNSREE.....PVSFDELTALQFASTAKYM 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	1686	100.0	2633	4	ABG06505	Abg06505 Novel hum
2	1686	100.0	2663	4	AAM39097	Aam39097 Human pol
3	1577.5	93.6	2688	4	AAM40883	Aam40883 Human pol
4	1258.5	74.6	2954	2	AAV01632	Aay01632 Amino aci
5	752	44.6	348	4	ABU53208	Abu53208 Human cel
6	752	44.6	366	4	ABU53125	Abu53125 Intracell
7	688	40.8	2013	4	ABB62322	Abb62322 Drosophil
8	643	38.1	473	5	ABG70992	Abg70992 Human tar
9	643	38.1	522	5	ABG70991	Abg70991 Human HSK
10	643	38.1	1232	7	ADL49938	Add49938 Human lun
11	643	38.1	1232	7	ADL18924	Add18924 Human dis
12	633	37.5	1232	7	ADL49937	Add49937 Human kin
13	633	37.5	1232	7	ADL49932	Add49932 Human lun
14	627.5	37.2	677	4	ABB65183	Abb65183 Drosophil
15	627	37.2	1232	5	ABG70990	Abg70990 Human HSK
16	626	37.1	1234	5	ABG70993	Abg70993 Human HSK
17	624.5	37.0	1029	5	AAE17786	Aae17786 Human kin
18	624.5	37.0	1029	7	ADL10190	Adl10190 Human NOV
19	620.5	36.8	329	5	AAE17787	Aae17787 Human kin
20	618.5	36.7	1034	3	AAE17787	Aae17787 Human kin
21	618.5	36.7	1069	3	AAE17787	Aae17787 Human kin
22	618.5	36.7	1121	3	AAE17787	Aae17787 Human kin
23	613.5	36.4	1038	5	AAE17787	Aae17787 Human kin
24	597	35.4	784	2	AAE17787	Aae17787 Human kin
25	595	35.3	1921	4	ABB62962	Abb62962 Drosophil

ALIGNMENTS

RESULT 1

ABG06505

ID ABG06505 standard; protein; 2633 AA.

XX AC ABG06505;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #6496.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS70692.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 36864; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging

Abg20649 Novel hum
Aaw72745 Drosophil
Aaw72744 Drosophil
Aaw72746 Drosophil
Abb63485 Drosophil
Abb67088 Kinesin h
Aae14401 Human HSK
Aae14402 Human HSK
Aau79592 Human HSK
Aae14400 Human kin
Aau79590 Human kin
Aab48222 Human bla
Abd80468 Ovarian c
Adc35116 Human bre
Aab67093 Kinesin h
Aau19569 Human dia
Abp51294 Human MDD
Ade55349 Rat Prote
Aau74840 Human HSK
Abp68930 Human pol

CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences
XX
XX
SQ Sequence 2633 AA;

Query Match 100.0%; Score 1686; DB 4; Length 2633;
Best Local Similarity 100.0%; Pred. No. 1.3e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEEGAVAVCVVRPLNSREESLGETAQYVWKTNNVIYQVDGSKSFNDRVPHGNETKN 60
DB 2 AEEGAVAVCVVRPLNSREESLGETAQYVWKTNNVIYQVDGSKSFNDRVPHGNETKN 61

QY 61 VVEETAAPLIIDSAIQGYNGTTFAYGQTASGKTYTMMGSEDLGVIPRAIHDFQIKKFP 120
DB 62 VVEETAAPLIIDSAIQGYNGTTFAYGQTASGKTYTMMGSEDLGVIPRAIHDFQIKKFP 121

QY 121 DREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNRYVADLTEEVYVTSMAK 180
DB 122 DREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNRYVADLTEEVYVTSMAK 181

QY 181 ITKGEKSHYGETKNQSRSSHTIFRMILSRKEGPEPNCESGVKVSHLNLDLAGSR 240
DB 182 ITKGEKSHYGETKNQSRSSHTIFRMILSRKEGPEPNCESGVKVSHLNLDLAGSR 241

QY 241 AAQTGAAGVRLKEGCNINRSLFILGVIKKLSDGQVGGFINYRDSKLTILQNSLGNPK 300
DB 242 AAQTGAAGVRLKEGCNINRSLFILGVIKKLSDGQVGGFINYRDSKLTILQNSLGNPK 301

QY 301 TRIICTITPVSFDETLTALQFASTAKYM 328
DB 302 TRIICTITPVSFDETLTALQFASTAKYM 329

RESULT 3
AAM39097
ID AAM39097 standard; protein; 2663 AA.
AC AAM39097;
XX
DT 22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 2242.

Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX WPI, 2001-442253/47.
DR N-PSDB; AAI58253.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 2242; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the
encoded polypeptides (AAM38642-AAM42213) with neotropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: Immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
C.N.S disorders. Note: The sequence data for this patent did not form
part of the printed specification
XX
SQ Sequence 2663 AA;

Query Match 100.0%; Score 1686; DB 4; Length 2663;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEEGAVAVCVVRPLNSREESLGETAQYVWKTNNVIYQVDGSKSFNDRVPHGNETKN 60
DB 2 AEEGAVAVCVVRPLNSREESLGETAQYVWKTNNVIYQVDGSKSFNDRVPHGNETKN 61

QY 61 VVEETAAPLIIDSAIQGYNGTTFAYGQTASGKTYTMMGSEDLGVIPRAIHDFQIKKFP 120
DB 62 VVEETAAPLIIDSAIQGYNGTTFAYGQTASGKTYTMMGSEDLGVIPRAIHDFQIKKFP 121

QY 121 DREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNRYVADLTEEVYVTSMAK 180
DB 122 DREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNRYVADLTEEVYVTSMAK 181

QY 181 ITKGEKSHYGETKNQSRSSHTIFRMILSRKEGPEPNCESGVKVSHLNLDLAGSR 240
DB 182 ITKGEKSHYGETKNQSRSSHTIFRMILSRKEGPEPNCESGVKVSHLNLDLAGSR 241

QY 241 AAQTGAAGVRLKEGCNINRSLFILGVIKKLSDGQVGGFINYRDSKLTILQNSLGNPK 300
DB 242 AAQTGAAGVRLKEGCNINRSLFILGVIKKLSDGQVGGFINYRDSKLTILQNSLGNPK 301

QY 301 TRIICTITPVSFDETLTALQFASTAKYM 328
DB 302 TRIICTITPVSFDETLTALQFASTAKYM 329

RESULT 3
AAM40883
ID AAM40883 standard; protein; 2688 AA.
XX
AC AAM40883;
XX
DT 22-OCT-2001 (first entry)

Query Match	93.6%;	Score 1577.5;	DB 4;	Length 2688;
Best Local Similarity	95.2%;	Pred. No. 6.5e-145;		
Matches 315;	Conservative	2;	Mismatches 11;	Indels 3;
Gaps	3;			
1	AEEGAVACVRVRLNLSREESLGETAQVYVTKTDNNVYQVDSKSFNFDVFGHNETTKN	60		
23	AEEGAVACVRVRLNLSREESLGETAQVYVTKTHNNVYVDSKSFNFDVFLHGNETPKN	82		
61	VVEETAAPLIDSAIOGYNGTIFPAYQOTASGKTYTMGSEDHGLGVIPRA-IHDIF-QKIKX	118		
83	VVEETAAPLIDSAIOGYNGTIFPAYQOTASGKTYTMGSEDHGLGVIPQGFHGSQIXE	142		
119	-FPDREFLLRVSMYEINTEITDILCGTQKMKPLIIRDVNRNVYVADLTTEEVYVYSEMA	177		

```
Best Local Similarity 73.4%; Pred. No. 1.8e-113;
Matches 243; Conservative 40; Mismatches 43; Indels 5; Gaps 2;

QY 1 AEEGAVACVVRPLNSREESLGETAQVYWKTDNNVIYQVDGSKSFNDFRVFHNETHKN 60
Db 2 SEGDAVKCVVRPLIOREQ--GDOANLQWAGNNTISQVDGYSFNFDRVFNSEHSTSQ 59
QY 61 VYEEIAPIIDSIAIQYNGTIFAYGQTASGTYTMMGSEDLHGVIPRAIHDIPOKIKKFP 120
Db 60 IYGEIAPVIRSAIQYNGTIFAYGQTSSGTYTMMGTPNSLGIPOAIOEVFKIIQEIF 119
QY 121 DREPLLRSYMEIYNETITDLCTQKMKPLIREDVNRNYYVADLTVEEVYTSEMALKW 180
Db 120 NREPLLRSYMEIYNETIVKOLLCDRRKKPLIREDENRNYYVADLTVEELVMVEHVIQW 179
QY 181 ITGKESRHYGETKMNQSRSSHTIFRMILESRKGEPS---NCEGSKYKSHLNLVDLAG 237
Db 180 IKGKKNRHYGETKMNDSRSHTIFRMIVESDRNDPTNSENCDGAVMVSHLNLVDLAG 239
QY 238 SERAAQTGAAGVRLKEGCNINRSLFILGOVTKKLSGQGVGFNRYRDSKLTRELONSLGG 297
Db 240 SERASQTGAEGVRLKEGCNINRSLFILGOVTKKLSGQAGGFNRYRDSKLTRELONSLGG 299
QY 298 NPKTRIICTTPVSFDETLTALQFASTAKYM 328
Db 300 NAKTVIICTTPVSFDETLTALQFASTAKGV 330

RESULT 5
ABUS3208
ID ABUS3208 standard; protein; 348 AA.
AC ABUS3208;
XX
DT 14-APR-2003 (first entry)
XX
DE Human cell cycle-associated DKFZphtes3_35b4 homologue #7.
XX
KW Human; gene therapy; vaccine; disease treatment; detection.
XX
OS Homo sapiens.
XX
FN WO200112659-A2.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-IB001496.
XX
PR 18-AUG-1999; 99US-0149499P.
PR 28-SEP-1999; 99US-0156503P.
XX
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
PI Wiemann S;
XX
DR WPI; 2001-327840/34.
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies.
XX
PS Example III; Page 829; 1095pp; English.
XX
CC This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence represents a homologue
CC of a polypeptide described in the disclosure of the invention
XX
```

```
SQ Sequence 348 AA;
Query Match 44.6%; Score 752; DB 4; Length 348;
Best Local Similarity 51.2%; Pred. No. 4.9e-65;
Matches 173; Conservative 36; Mismatches 103; Indels 26; Gaps 7;

QY 11 RVPLNSREESLGETAQVYVW-----KTDNNVIYQVDGSKSFNDFRVFHNETHKNYEE 64
Db 1 RCPFLNREINDGSCVQVQPPWTGYKTVHNGHEGDSPHKSFTHFVFWNCTQEDVYDT 60
QY 65 IAAPIDSALQYNGTIFAYGQTASGTYTMMG-----SEDLGVIPRAIHDIPOKIKKFP 120
Db 61 VAHPVIDDCFHGYNCTIFAYGQTSGKTYTMMGGSEHDPHMGIIIPCCDHIDFRIIDKFQ 120
QY 121 DRE---FLLRVSYMEIYNETITDLIC-GTQMKPLIREDVNRNYYVADLTVEEVYTSEM 176
Db 121 EKQDHFVHKVCSYMEIYNEIYDILLCPNQHMKPLNIEHPNMGPPYQGCTEPHVCSEYD 180
QY 177 ALKMWITKESRHYGETKMNQSRSSHTIFRMILESRKGEPSNCEGSKYKSHLNLVDLA 236
Db 181 ACHWIQGNKRNHVAATNMNDHSSRSHTIFTIRVEQRHK---QCDHEHVCCHKMNLVDLA 236
QY 237 GSEAAQTGAAGVRLKEGCNINRSLFILGOVTKKLSGQV-----GGFINYRDSKLTREL 290
Db 237 GSERVNETGAGQRLKEGCNINOSLTTLGNVINALADGQTKMYTGGHGHIPYRDSKLTWL 296
QY 291 LONSLGNPKTRIICTTPV--SPDETTLTALQFASTAK 326
Db 297 LQDSLGNCKTCMIACIWPADWNYEETLSTLRYADRAK 334

RESULT 6
ABUS3125
ID ABUS3125 standard; protein; 366 AA.
AC ABUS3125;
XX
DT 15-APR-2003 (first entry)
XX
DE Intracellular trafficking-associated DKFZphtes3_26g22 homologue #2.
XX
KW Human; gene therapy; vaccine; disease treatment; detection.
XX
OS Homo sapiens.
XX
FN WO200112659-A2.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-IB001496.
XX
PR 18-AUG-1999; 99US-0149499P.
PR 28-SEP-1999; 99US-0156503P.
XX
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
PI Wiemann S;
XX
DR WPI; 2001-327840/34.
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies.
XX
PS Example III; Page 745; 1095pp; English.
XX
CC This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence represents a homologue
CC of a polypeptide described in the disclosure of the invention
XX
```

CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention
 XX Sequence 366 AA;
 SQ Query Match 44.6%; Score 752; DB 4; Length 366;
 Best Local Similarity 51.2%; Pred. No. 5.3e-65;
 Matches 173; Conservative 36; Mismatches 103; Indels 26; Gaps 7;
 QY 11 RVRPLNREESLGETAQYVW-----KTDNNVIYQVDSKSFNDFRPHGNETTKNVEE 64
 DB 1 RCRPLNREINDGSCVQVWPWTGYKTVNGHEDSPHKSTFDHVFWMNCTQEDVYDT 60
 QY 65 IAPIIDSAIQGYNGTIFAYGQTASGKTYTMWG-----SEDLGVIPRAIHDFQKIKKFP 120
 DB 61 VAHPIDVDCFHGYNCTIFAYGQTSGKTYTMWGPGEHPDHMGIIIRCCCHDIFRIDKFQ 120
 QY 121 DRE---FLLRVSMEIYNETITDLC-GTQMKPLIREDVNRNYYVADLTERVVTSEM 176
 DB 121 EKDHDFHWKCSMEIYNEEYDLCNPOHMKPLNIHEHPNMGPIYVQGTETFEHVCSED 180
 QY 177 ALKWITKESRHYGETKMNQSRSHRTIFRMILESREKGEPSNCEGSKVSHLNLVDLA 236
 DB 181 ACHWIWQGNKRHVAATNMNDHSSRSHRTIFTIHVEQRHK-----QCDEHVCHSKMNLVDLA 236
 QY 237 GSRAAQTGAAGVRLKEGCNINRSLFILGVQVKKLSGQV-----GGFINYRDSKLTRI 290
 DB 237 GSERVARTGAEGRLKEGCNINSLATLGNVINADGQTKYMYGGHPIPYRDSKLTLWL 296
 QY 291 LQNSLGNPKTRITCTIPV--SFDETLTALQFASTAK 326
 DB 297 LQDSLGNCKTMIACIWPADWNYEETLSTIRYADRAK 334
 RESULT 7
 ABB62322
 ID ABB62322 standard; protein; 2013 AA.
 XX AC ABB62322;
 DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 13758.
 XX DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS Drosophila melanogaster.
 PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX PI WPI; 2001-656860/75.
 DR N-PSDB; ABL06425.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Disclosure; SEQ ID NO 13758; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABBS72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 2013 AA;
 SQ Query Match 40.8%; Score 688; DB 4; Length 2013;
 Best Local Similarity 49.8%; Pred. No. 1.3e-57;
 Matches 162; Conservative 48; Mismatches 99; Indels 16; Gaps 8;
 QY 5 AVAVCVRVRLNREESLGETAQYVWKT--DNNVIYQVDSKSFNDFRPHGNETTKNVEE 62
 DB 8 SIQVCIKVRPCPEGLTSL-----WQVKERSHLADSHAEPVYDFYDEGASNOEVF 60
 QY 63 EETAAPIDSAIQGYNGTIFAYGQTASGKTYTMWGSEDLGLVIPRAIHDFQKIKKFPDR 122
 DB 61 DRWAKHIVHACMQGFNGTIFAYGQTSGKTYTMWGDEQNPVMVLAKEIFQIISSETER 120
 QY 123 EFLLRVSMEIYNETITDLCGTQMKPLIREDVNRNYYVADLTERVVTSEM-ALKWI 181
 DB 121 DFLRVGYIIEYNEKIYDILL--NKNQDLKHESGNGIVNWN--CEECITITSEVDLRL 176
 QY 182 TKGEKSRHYGETKMNQSRSHRTIFRMILESREKGEPSNCEGSKVSHLNLVDLAGSERA 241
 DB 177 CLGNKERTVGETNMNRSRSHAFKIIIESR-KSHSD--DDAVIOSVLNVDLAGSERA 234
 QY 242 AQTGAAGVRLKEGCNINRSLFILGVQVKKLSGQVGFINYRDSKLTRIQLNSLGGNPKT 301
 DB 235 DQTGARGARLKEGGINKSLLSNVIKLSLENADNRFTNYRDSKLTRIQLNSLGGNPKT 294
 QY 302 RIICITIPVSFDETLTALQFASTAK 326
 DB 295 SIICITIKPIMEESOSTLSFATRAK 319
 RESULT 8
 ABB70992
 ID ABB70992 standard; protein; 473 AA.
 XX AC ABB70992;
 DT 10-DEC-2002 (first entry)
 XX DE Human target protein.
 XX DE Microtubule stimulated ATPase; cellular proliferation; cancer; AIDS;
 KW hyperplasia; restenosis; cardiac hypertrophy; immune disorder; HIV;
 KW inflammation; autoimmune disease; arthritis; graft rejection; psoriasis;
 KW inflammatory bowel disease; proliferation; medical procedure; surgery;
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;
 XX angioplasty; human; Hskif; kinesin family.
 OS Homo sapiens.
 XX US6440684-B1.
 XX PD 27-AUG-2002.
 XX PF 12-JUN-2000; 2000US-00592054.
 XX PR 12-JUN-2000; 2000US-00592054.
 XX PA (CYTO-) CYTOKINETICS INC.
 XX PI Beraud C, Finer JT, Sakowicz R, Wood KW;
 XX WPI; 2002-711529/77.
 DR N-PSDB; ABS55162.

XX Screening for modulators of target protein having microtubule stimulated
PT ATPase activity e.g. kinesin family of protein, useful for treating
PT cancer, psoriasis, arthritis, human immunodeficiency virus (HIV)
PT infection.
XX
XX Claim 3; Fig 6; 34pp; English.
XX
XX The present invention relates to a new method of screening modulators of
CC target protein with microtubule stimulated ATPase activity. The method
CC involves contacting the target protein with an agent at 1st and 2nd
CC concentrations and determining the level of activity (e.g. binding or
CC ATPase activity) of target protein, where a difference between levels of
CC activity of target protein contacted with 1st and 2nd concentrations of
CC an agent indicates that an agent modulates activity of target protein.
CC The invention can be used for screening for modulators of target protein
CC having microtubule stimulated ATPase activity. The compounds identified
CC by method of the invention are useful for treating cellular proliferation
CC including cancer, hyperplasias, restenosis, cardiac hypertrophy, immune
CC disorders and inflammation. The compounds identified by the method are
CC also useful for treating autoimmune disease, arthritis, graft rejection,
CC inflammatory bowel disease, proliferation induced by medical procedures,
CC e.g. surgery, angioplasty etc. The compounds are also useful for treating
CC psoriasis. The compounds are useful for inhibiting human immunodeficiency
CC virus (HIV) and thus treating acquired immunodeficiency syndrome (AIDS).
CC The present amino acid sequence represents the human target protein of
CC the invention
XX
XX SQ Sequence 473 AA;
Query Match 38.1%; Score 643; DB 5; Length 473;
Best Local Similarity 44.4%; Pred. No. 4.7e-54;
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;
QY 6 VAVCVVRPLNREESLG-ETAQVYWKTDNNVIYQVDSKSFNDRVPHGNETTKVYEE 64
DB 8 VRVALRCRPLVPKTEISEGCMCLSFVPGEPQVVGTD--KSTYDFVDPSTEQEEVENT 65
QY 65 IAAPITDSAIQNGTIFAYGQTASGKTWTMMG-----SEDHLGVIPRAIHDFQKIK 117
DB 66 AVAPLIKGVFKGNATVLAIGTGGKYSGMGAYTAEQENETVGVIPRVQLLFKEID 125
QY 118 KPDPREFLLRVSYMEIYNETITDLCGQTKMKPLIREDVNRNVVADLTBEVYVSEMA 177
DB 126 KKSDFEFTLKVSYLEINEEILDLCPREKAQINREDPKGKIVGLTEKTVLVALDT 185
QY 178 LKWIYTKGSRHYGETKNNQSRSHITPMTLESREKGEPCNCGSVKVSHLNLDLAG 237
DB 186 VSCLEQGNNSRTVASTAMNSQSSRSHAITISLEORKSD----KNSFRSKHLVDLAG 241
QY 238 SERAAQTGAAGVRLKEGNCINRSLFTLGQVVKLSGQGVGFYNYRDSKLTILQNSLGG 297
DB 242 SERQKTKAEGRLKEGININRGLLCLGNVISALGDGDKKGGFVYRDSKLTLLQDSLGG 301
QY 298 NPKTRICTITPV--SFDFTLALQASTAK 326
DB 302 NSHTLMIACVSPADSNLEETLNTLRVADRAR 332
RESULT 9
ID ABG70991 standard; protein; 522 AA.
XX ABG70991;
AC ABG70991;
XX
XX 10-DEC-2002 (first entry)
XX
XX Human HsKif4 construct protein.
XX
XX Microtubule stimulated ATPase; cellular proliferation; cancer; AIDS;
XX hyperplasia; restenosis; cardiac hypertrophy; immune disorder; HIV;
XX inflammation; autoimmune disease; arthritis; graft rejection; psoriasis;
XX inflammatory bowel disease; proliferation; medical procedure; surgery;
XX

human immunodeficiency virus; acquired immunodeficiency syndrome;
angioplasty; human; HsKif4; kinesin family.
Homo sapiens.
Key Location/Qualifiers
Region 1..22
Region /note= "N-terminal T7 epitope"
Region 436..516
Region /note= "C-terminal myc epitope"
Region 517..522
Region /note= "6-histidine residues at C-terminus"
US6440684-B1.
27-AUG-2002.
12-JUN-2000; 2000US-00592054.
12-JUN-2000; 2000US-00592054.
(CYTO-) CYTOKINETICS INC.
Beraud C, Finer JT, Sakowicz R, Wood KW;
WPI: 2002-711529/77.
N-PSDB; ABS55161.
Screening for modulators of target protein having microtubule stimulated
ATPase activity e.g. kinesin family of protein, useful for treating
cancer, psoriasis, arthritis, human immunodeficiency virus (HIV)
infection.
Claim 2; Fig 4; 34pp; English.
The present invention relates to a new method of screening modulators of
target protein with microtubule stimulated ATPase activity. The method
involves contacting the target protein with an agent at 1st and 2nd
concentrations and determining the level of activity (e.g. binding or
ATPase activity) of target protein, where a difference between levels of
activity of target protein contacted with 1st and 2nd concentrations of
an agent indicates that an agent modulates activity of target protein.
The invention can be used for screening for modulators of target protein
having microtubule stimulated ATPase activity. The compounds identified
by method of the invention are useful for treating cellular proliferation
including cancer, hyperplasias, restenosis, cardiac hypertrophy, immune
disorders and inflammation. The compounds identified by the method are
also useful for treating autoimmune disease, arthritis, graft rejection,
inflammatory bowel disease, proliferation induced by medical procedures,
e.g. surgery, angioplasty etc. The compounds are also useful for treating
psoriasis. The compounds are useful for inhibiting human immunodeficiency
virus (HIV) and thus treating acquired immunodeficiency syndrome (AIDS).
The present amino acid sequence represents the human HsKif4 (kinesin
family) construct protein of the invention
Sequence 522 AA;
Query Match 38.1%; Score 643; DB 5; Length 522;
Best Local Similarity 44.4%; Pred. No. 4.7e-54;
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;
QY 6 VAVCVVRPLNREESLG-ETAQVYWKTDNNVIYQVDSKSFNDRVPHGNETTKVYEE 64
DB 30 VRVALRCRPLVPKTEISEGCMCLSFVPGEPQVVGTD--KSTYDFVDPSTEQEEVENT 87
QY 65 IAAPITDSAIQNGTIFAYGQTASGKTWTMMG-----SEDHLGVIPRAIHDFQKIK 117
DB 88 AVAPLIKGVFKGNATVLAIGTGGKYSGMGAYTAEQENETVGVIPRVQLLFKEID 147
QY 118 KPDPREFLLRVSYMEIYNETITDLCGQTKMKPLIREDVNRNVVADLTBEVYVSEMA 177
DB 148 KKSDFEFTLKVSYLEINEEILDLCPREKAQINREDPKGKIVGLTEKTVLVALDT 207

XX	PD	06-MAR-2003.	XX	DT	15-JAN-2004 (first entry)
XX	PF	23-AUG-2002; 2002WO-GB003892.	XX	DE	Human kinesin family member 4A.
XX	PR	23-AUG-2001; 2001GB-00020558.	XX	KW	Human; lung cancer antigen; cytostatic; lung cancer; gene therapy;
XX	PR	05-OCT-2001; 2001GB-00024037.	XX	KW	vaccine; T-cell; tumour.
XX	PA	(OXFO-) OXFORD BIOMEDICA UK LTD.	XX	OS	Homo sapiens.
XX	PI	Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;	XX	PN	US2003194764-A1.
XX	DR	WPI; 2003-230046/28.	XX	XX	16-OCT-2003.
XX	DR	N-PSDB; ADD18925.	XX	PD	04-APR-2002; 2002US-00116712.
XX	XX	New substantially purified polypeptide, useful for diagnosing or treating	XX	PF	05-APR-2001; 2001US-0282289P.
PT	PT	a hypoxia-regulated condition, such as cancer, ischemia, reperfusion	XX	PR	05-OCT-2001; 2001US-0327511P.
PT	PT	injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or	XX	XX	(CORI-) CORIXA CORP.
PT	PT	wound healing.	XX	PA	Bangur CS, Switzer A;
XX	PS	Claim 25; SEQ ID NO 413; 424pp; English.	XX	PI	WPI; 2003-844452/78.
XX	XX	This invention relates to novel human genes and gene product which are	XX	DR	N-PSDB; ADD49935.
CC	CC	implicated in certain disease states. Compounds which modulate the	XX	XX	New isolated polypeptides and polynucleotides useful for diagnosing,
CC	CC	proteins of the invention may have cytostatic, antiinflammatory, the	XX	PT	preventing and treating cancer, particularly lung cancer.
CC	CC	ophthalmological, antiarteriosclerotic or vulnerary activities. The	XX	PT	Example 3; SEQ ID NO 669; 250pp; English.
CC	CC	sequences of the invention may be useful for gene therapy. The invention	XX	XX	The invention relates to an isolated polynucleotide (a) comprising any of
CC	CC	may be useful for diagnosing or treating a hypoxia-regulated condition,	XX	XX	the 666 fully defined nucleotide sequences appearing as ADD49269 -
CC	CC	such as tumorigenesis, angiogenesis, apoptosis, inflammation,	XX	XX	ADD49935, ADD49936 and ADD49938, complements of (a); sequences of at
CC	CC	erythropoiesis, or the biological response to hypoxia conditions	XX	XX	least 20 contiguous residues of (a); sequences that hybridise to (a)
CC	CC	including processes such as glycolysis, gluconeogenesis, glucose	XX	XX	under highly stringent conditions; sequences having at least 75 or 90%
CC	CC	transportation, catecholamine synthesis, iron transport or nitric oxide	XX	XX	identity to (a); or degenerate variants of (a). Also included are an
CC	CC	synthesis. The disease includes cancer, ischaemic conditions, reperfusion	XX	XX	isolated polypeptide (b) (comprising: sequences encoded by the new
CC	CC	injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,	XX	XX	polynucleotide; any of the 4 amino acid sequences fully defined in the
CC	CC	inflammatory conditions or wound healing. The present sequence is that of	XX	XX	specification; or sequences having at least 70 or 90% identity to the
XX	XX	a disease related protein of the invention.	XX	XX	sequence in (a) or (b)), an expression vector comprising the above
XX	XX	Sequence 1232 AA;	XX	XX	polynucleotide operably linked to an expression control sequence, a host
Query Match	38.1%; Score 643; DB 7; Length 1232;		XX	XX	cell transformed or transfected with the above expression vector, an
Best Local Similarity	44.4%; Pred. No. 1.7e-53;		XX	XX	isolated antibody, or its antigen-binding fragment, that specifically
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;			XX	XX	binds to the above polypeptide, an oligonucleotide that hybridises to the
QY	6 VACVVRPLNSREESLG-ETAAQVYKTDNNVIYQVDSKSPFNFRVPHGNETTKNYYEE 64		XX	XX	above-mentioned nucleotide sequences under highly stringent conditions, a
Db	10 VRVALRCRPLVPKEISEGCMCLSFVPGEPQVVVGTD--KSFTYDFVDPSTEQEEVFNT 67		XX	XX	fusion protein comprising at least one polypeptide cited above, detecting
QY	65 IAAPLIDSAIQYNGTIFAYGOTAGSKTYWVG-----SEDHLGVIPRAITHDIFQKIK 117		XX	XX	the presence of a cancer in a patient (comprising: obtaining a biological
Db	68 AVAPLIKGVFKGYNATVLAIGTGSGKTYSMGGATVTAQENEPPTVGVIPRVLIQLFKEID 127		XX	XX	sample from the patient; contacting the biological sample with a binding
QY	118 KPPDEFILRVSYMETINETIIDLGGTQMKPLIREDVNRNVVADLTEEVVYTSEMA 177		XX	XX	agent that binds to the polypeptide, or with the oligonucleotide cited
Db	128 KKSDFEFLKVSYLEIYNEIIDLCPSEKAQINIREDPKEGKIVGLTETVLVADLT 187		XX	XX	above; detecting in the sample an amount of the polypeptide that binds to
QY	178 LKWITKGEKSRHYGETKMNORSRSHITIFRMILESEKPEPCNCGSVKVSHLNVLADLAG 237		XX	XX	the binding agent, or an amount of a polynucleotide that hybridises to
Db	188 VSCLEQGNNSRTVASTAMNSQSRSRSHAFITISLEQRKSD----KNSFRSKLHLVDLAG 243		XX	XX	the oligonucleotide; and comparing the amount of polypeptide, or
QY	238 SERAQGTGAAGVRLKEGCMINRSLFTLGOVKKLSDGQVGGFTINVRDSKLTILQNSLGG 297		XX	XX	polynucleotide that hybridises to the oligonucleotide, to a predetermined
Db	244 SERQKTKAEGDKRLKEGININRGLLCGNVISAIGDDKKGGVFPVDRDSKLTILLQDSLGG 303		XX	XX	cut-off value and then determining the presence of a cancer in the
QY	298 NPKTRITCITPV--SFDETLTALOPASTAK 326		XX	XX	patient), a method for stimulating and/or expanding T-cells specific for
Db	304 NSHTLMACVSPADSNLEETLNLRYADRAR 334		XX	XX	a tumour protein (comprising contacting T-cells with the above
RESULT 12			XX	XX	polypeptide, polynucleotide or antigen-presenting cells that express the
ADD49937			XX	XX	polypeptide, under conditions and for a time sufficient to permit the
ID ADD49937 standard; protein; 1232 AA.			XX	XX	stimulation and/or expansion of T-cells), an isolated T-cell population
XX			XX	XX	comprising T-cells prepared by the method, a composition comprising a
AC			XX	XX	first component selected from physiological carriers and
			XX	XX	immunostimulants, and a second component selected from the above
			XX	XX	polypeptide, polynucleotide, antibody, fusion protein, T-cell population
			XX	XX	and antigen-presenting cells that express the above polypeptide,
			XX	XX	stimulating an immune response in a patient (comprising administering to
			XX	XX	the patient the above composition) treating lung cancer in a patient
			XX	XX	(comprising administering to the patient the above composition and a
			XX	XX	diagnostic kit (comprising: at least one oligonucleotide cited above; or
			XX	XX	at least one antibody cited above and a detection reagent, where the
			XX	XX	detection reagent comprises a reporter group). The composition and
			XX	XX	methods are useful in diagnosing, preventing and treating cancer,
			XX	XX	particularly lung cancer. The present sequence is a lung cancer-


```
CC associated antigen of the invention.
XX SQ Sequence 1232 AA;

Query Match      37.5%; Score 633; DB 7; Length 1232;
Best Local Similarity 44.4%; Pred. No. 1.6e-52;
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 6;

QY 6 VAVCVVRPLNSREESLG-ETAQVYWKTDNNVIYQVDSKSFNDRVFGHNETTKNVYEE 64
DQ 10 VRVALRCRPLVPKEISEGCMCLSFVPGEPQVVVGTD--KSFTYDFVDPSTQEVFNT 67
QY 65 IAAPIIDSAIOGYNGTIFAYGQTASGKTYTMWG-----SEDLGVIPRAIHDFOKIK 117
DQ 68 AVAPLIKGVFKGNATVLAAYGTGSGKTYSMGGAYTAQENEPVGVIPRVQLLFKEID 127
QY 118 KFPDRFLLRVSYMEIYNETITDLLCGTKMKPLIREDVNRVYVADLTVEVYVTEMA 177
DQ 128 KKSDFEFTLVKSYLEIYNEEILDLCPREKAQINREDPKGKIVGLTEKTVLVALDT 187
QY 178 LKWITKGEKSRHYGETKMNQSRSSHTIFRMILSRKGEPSNCEGSKVSHNLVLDLAG 237
DQ 188 VSCLEQGNNSRTVASTAMNSQSSRSHAFIT---SLEQKSKDNSSFR-SKLHLVDLAG 243
QY 238 SERAAQTGAAGVRLKEGCNINRSLFILGQVKKLSGQGVGFINYRDSKLTIRLQNSLGG 297
DQ 244 SEROKTKAEGDRLKEGININRGLLCGNVISALGDDKKGGFAPYRDSKLTIRLQDSLGG 303
QY 298 NPKTRIICITPV--SFDETLTALQFASTAK 326
DQ 304 NSHTLMACVSPADSNLEETLTLRYADRAR 334

RESULT 13
ID ADD49932
XX ADD49932 standard; protein; 1232 AA.
AC ADD49932;
XX
XX 15-JAN-2004 (first entry)
XX Human lung specific tumour antigen L 1477p.
DE Human; lung cancer antigen; cytostatic; lung cancer; gene therapy;
KW vaccine; T-cell; tumour.
XX
XX Homo sapiens.
XX US2003194764-A1.
XX PD 16-OCT-2003.
XX
XX 04-APR-2002; 2002US-00116712.
XX
XX 05-APR-2001; 2001US-0282289P.
XX
XX 05-OCT-2001; 2001US-0327511P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Bangor CS, Switzer A;
XX
XX WPI; 2003-844452/78.
XX
XX N-PSDB; ADD49929.
XX
XX New isolated polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cancer, particularly lung cancer.
XX
XX Example 3; SEQ ID NO 664; 250pp; English.
XX
XX The invention relates to an isolated polynucleotide (a) comprising any of
XX the 666 fully defined nucleotide sequences appearing as ADD49269 -
XX ADD49935, ADD49936 and ADD49938, complements of (a); sequences of at
XX least 20 contiguous residues of (a); sequences that hybridise to (a)
```


1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1686	100.0	2662	4	US-09-595-684B-31		Sequence 31, Appl
2	1258.5	74.6	2954	4	US-09-150-867-1		Sequence 1, Appl
3	643	38.1	473	4	US-09-592-054-6		Sequence 6, Appl
4	643	38.1	522	4	US-09-592-054-4		Sequence 4, Appl
5	633	37.5	1231	4	US-09-595-684B-23		Sequence 23, Appl
6	627	37.1	1232	4	US-09-592-054-2		Sequence 2, Appl
7	626	37.2	1234	4	US-09-592-054-8		Sequence 8, Appl
8	593.5	35.2	411	2	US-08-713-815A-4		Sequence 4, Appl
9	593.5	35.2	441	2	US-08-713-815A-3		Sequence 3, Appl
10	593.5	35.2	975	4	US-09-914-259-19		Sequence 19, Appl
11	592	35.1	375	4	US-09-572-191-4		Sequence 4, Appl
12	592	35.1	375	4	US-09-723-262-4		Sequence 4, Appl
13	592	35.1	375	4	US-09-723-219-4		Sequence 6, Appl
14	592	35.1	409	4	US-09-572-191-6		Sequence 6, Appl
15	592	35.1	409	4	US-09-723-262-6		Sequence 2, Appl
16	592	35.1	409	4	US-09-723-262-6		Sequence 2, Appl
17	592	35.1	1388	4	US-09-572-191-2		Sequence 2, Appl
18	592	35.1	1388	4	US-09-723-262-2		Sequence 2, Appl
19	592	35.1	1388	4	US-09-723-219-2		Sequence 2, Appl
20	591.5	35.1	1031	4	US-09-914-259-24		Sequence 24, Appl
21	583	34.6	963	4	US-09-914-259-22		Sequence 22, Appl
22	582	34.5	928	4	US-09-914-259-23		Sequence 23, Appl
23	582	34.5	963	4	US-09-914-259-20		Sequence 20, Appl
24	582	34.5	1066	3	US-09-541-782-8		Sequence 8, Appl
25	582	34.5	1066	4	US-09-723-820-8		Sequence 8, Appl
26	582	34.5	1066	4	US-10-270-085-8		Sequence 8, Appl
27	580.5	34.4	1032	4	US-09-914-259-26		Sequence 26, Appl

```
QY 301 TRIICITPVSPFDEITLALQFASTAKYM 328
Db 302 TRIICITPVSPFDEITLALQFASTAKYM 329

RESULT 2
US-09-150-867-1
; Sequence 1, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/09/150,867
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/058,645
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 2954
; TYPE: PRT
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: Xenopus centromere-associated protein-B (XCENP-B)
; OTHER INFORMATION: member of the kinesin superfamily of microtubule
; OTHER INFORMATION: motor proteins
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(472)
; OTHER INFORMATION: kinesin like motor domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (473)..(2752)
; OTHER INFORMATION: rod domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2753)..(2954)
; OTHER INFORMATION: tail domain
US-09-150-867-1

Query Match 74.6%; Score 1258.5; DB 4; Length 2954;
Best Local Similarity 73.4%; Pred. No. 6.4e-124;
Matches 243; Conservative 40; Mismatches 43; Indels 5; Gaps 2;

QY 1 APEGAVAVCVVRPLNSREESLG-ETAQVYWKTDNNVYQVDSKSFNEDRVPHGNETTKYN 60
Db 2 SEGDAVKVCVRPLIQREQ--GDQANLQWKAGNNTISQVDGTSKSFNEDRVFNESHSTSQ 59

QY 61 VYEEIAPIIDSALIOGYNGTIFAYGQTASGKTYTMMGSEDLHLGVIPRAIHDFQKIKKPP 120
Db 60 IYQEIAPVPIRSALQGYNGTIFAYGQTSSGKTYTMMGTNSGLIIPQALQEFVKLIQETP 119

QY 121 DREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNVYVADLTTEEYVVTSEMAKW 180
Db 120 NREFLLRVSYMEIYNETVVDLLCDDRKKPLEIREDFNRNVYVADLTTELVMVPEHVIQW 179

QY 181 ITKGEKSRHYGETQNRSSRSHITFRMILESRKEGPEPS---NCEGSKVSHNLVLDLAG 237
Db 180 IKKGEKNRHYGETKMDHDSRSRSHITFRMIVESDRNDPTNSNCDCGAVMVSHNLVLDLAG 239

QY 238 SERAOTGAAGVRLKEGCNINRSFILQGVKIKLSDGVGGFYNIRDSKLTIRLQNSLGG 297
Db 240 SERASQTGAEGVRLKEGCNINRSFILQGVKIKLSDQAGGFYNIRDSKLTIRLQNSLGG 299

QY 298 NPKTRIICTITPV--SPDETTLALQFASTAKYM 328
Db 300 NAKTVIICTITPVSPFDEITLALQFASTAKHV 330

us-10-045-631b-88_copy_2_329.ra1

Query Match 38.1%; Score 643; DB 4; Length 473;
Best Local Similarity 44.4%; Pred. No. 1.1e-59;
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;

QY 6 VAVCVVRPLNSREESLG-ETAQVYWKTDNNVYQVDSKSFNEDRVPHGNETTKNVYEE 64
Db 8 VRVALRCRPLVPKEISEGCMCLSFVGPGEPOVVVGTD--KSFYDFVDFDPSTQEVEVNT 65

QY 65 IAAPIIDSALIOGYNGTIFAYGQTASGKTYTMMG-----SEDLHLGVIPRAIHDFQKIK 117
Db 66 AVAPLIKGVFKGYNATVLAQGTCGSKTYSMGAYTAEQENETGVGVIPRVIIQLLFKEID 125

QY 118 KFPDRFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNVYVADLTTEEYVVTSEMA 177
Db 126 KKSDFEFTLKVSYLEIYNERILDLCPREKAQINIREDPKKGKIVGLTEKTUVLUVALDT 185

QY 178 LKWITKGEKSRHYGETQNRSSRSHITFRMILESRKEGPEPSNCEGSKVSHNLVLDLAG 237
Db 186 VSCLEQGNNSRTVASTAMNSOSSRSHALFTISLEQRKSD---KNSSFRSKLHLVLDLAG 241

QY 238 SERAOTGAAGVRLKEGCNINRSFILQGVKIKLSDGVGGFYNIRDSKLTIRLQNSLGG 297
Db 242 SERQKTKAEGDRLKEGININRGLLCLGNVISALGDKKGGFVYRDSKLTIRLQNSLGG 301

QY 298 NPKTRIICTITPV--SPDETTLALQFASTAK 326
Db 302 NSHTLMIACVSPADSNLEETLNTLEYADRAR 332

RESULT 4
US-09-592-054-4
; Sequence 4, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684el motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592,054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Human
```

US-09-592-054-4

Query Match 38.1%; Score 643; DB 4; Length 522;
 Best Local Similarity 44.4%; Pred. No. 1.3e-59;
 Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;
 QY 6 VAVCVVRPLNSRESLG-ETAQVYWKTDNNVIVQDGSKSFNDRVPHGNETTKNVYEE 64
 DB 30 VRVALRCRPLVPKEISEGCMCLSFVPGEPQVVGTD--KSFTYDFVDPSTEQEEVNT 87
 QY 65 IAAPIDSAIQYNGTIFAYGQTASGKTYTMG-----SEDLGVIPRAIHDFOKIK 117
 DB 88 AVAPLKGVPKGNATVLAQGTGSKTYSMGAYTAQENEPVGVIPRVIQLLFKEID 147
 QY 118 KFPDREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNVVADLTTEEVTSEMA 177
 DB 148 KKSDFEFTLKVSYLEIYNEEILDLCPSREKAQINREDPKGKIVGLTEKTVLVALDT 207
 QY 178 LKWITKGEKSRHYGETKMNQSRSHITFRMILSRKGEPSNCEGSKVSHLNLVDLAG 237
 DB 208 VSCLEQGNNSRTVASTAMNSQSSRSHAFTI--SLEQKKSKDNSSPR-SKLHLVDLAG 263
 QY 238 SERAAQTGAAGVRLKEGNCINRSIFILGOVTKKLSGQVGFYNYRDSKLTRELQNSLGG 297
 DB 264 SERQKTKAEGDRKKEGININRGLLCLGNVISALGDDKGGFVYRDSKLTRELQNSLGG 323
 QY 298 NPKTRIICITTPV--SFDETLTALQFASTAK 326
 DB 324 NSHTLMIACVSPADSNLEETLNTLRYADRAR 354

RESULT 5

US-09-595-684B-23
 ; Sequence 23, Application US/09595684B
 ; Patent No. 6544766
 ; GENERAL INFORMATION:

; APPLICANT: Beraud, Christophe
 ; APPLICANT: Ohashi, Cara
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Vaisberg, Eugeni
 ; APPLICANT: Wood, Kenneth
 ; APPLICANT: Yu, Ming
 ; TITLE OF INVENTION: Human kinesins and methods of producing
 ; FILE OF INVENTION: and purifying human kinesins
 ; FILE REFERENCE: cytop036
 ; CURRENT APPLICATION NUMBER: US/09/595,684B
 ; PRIOR FILING DATE: 2002-06-24
 ; PRIOR APPLICATION NUMBER: 09/295,612
 ; PRIOR FILING DATE: 2000-04-20
 ; NUMBER OF SEQ ID NOS: 105
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 1231
 ; TYPE: PRT
 ; ORGANISM: Human

US-09-595-684B-23

Query Match 37.5%; Score 633; DB 4; Length 1231;
 Best Local Similarity 44.4%; Pred. No. 6e-58;
 Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 6;
 QY 6 VAVCVVRPLNSRESLG-ETAQVYWKTDNNVIVQDGSKSFNDRVPHGNETTKNVYEE 64
 DB 10 VRVALRCRPLVPKEISEGCMCLSFVPGEPQVVGTD--KSFTYDFVDPSTEQEEVNT 67
 QY 65 IAAPIDSAIQYNGTIFAYGQTASGKTYTMG-----SEDLGVIPRAIHDFOKIK 117
 DB 68 AVAPLKGVPKGNATVLAQGTGSKTYSMGAYTAQENEPVGVIPRVIQLLFKEID 127
 QY 118 KFPDREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNVVADLTTEEVTSEMA 177
 DB 128 KKSDFEFTLKVSYLEIYNEEILDLCPSREKAQINREDPKGKIVGLTEKTVLVALDT 187

QY 178 LKWITKGEKSRHYGETKMNQSRSHITFRMILSRKGEPSNCEGSKVSHLNLVDLAG 237
 DB 188 VSCLEQGNNSRTVASTAMNSQSSRSHAFTI--SLEQKKSKDNSSPR-SKLHLVDLAG 243
 QY 238 SERAAQTGAAGVRLKEGNCINRSIFILGOVTKKLSGQVGFYNYRDSKLTRELQNSLGG 297
 DB 244 SERQKTKAEGDRKKEGININRGLLCLGNVISALGDDKGGFVYRDSKLTRELQNSLGG 303
 QY 298 NPKTRIICITTPV--SFDETLTALQFASTAK 326
 DB 304 NSHTLMIACVSPADSNLEETLNTLRYADRAR 334

RESULT 6

US-09-592-054-2
 ; Sequence 2, Application US/09592054
 ; Patent No. 6440684
 ; GENERAL INFORMATION:

; APPLICANT: Beraud, Christophe
 ; APPLICANT: Finer, Jeffrey
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Wood, Kenneth
 ; TITLE OF INVENTION: No. 6440684el motor proteins and methods for
 ; FILE OF INVENTION: their use
 ; FILE REFERENCE: 1016
 ; CURRENT APPLICATION NUMBER: US/09/592,054
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1232
 ; TYPE: PRT
 ; ORGANISM: Human

US-09-592-054-2

Query Match 37.2%; Score 627; DB 4; Length 1232;
 Best Local Similarity 44.1%; Pred. No. 2.6e-57;
 Matches 146; Conservative 51; Mismatches 118; Indels 16; Gaps 6;
 QY 6 VAVCVVRPLNSRESLG-ETAQVYWKTDNNVIVQDGSKSFNDRVPHGNETTKNVYEE 64
 DB 10 VRVALRCRPLVPKEISEGCMCLSFVPGEPQVVGTD--KSFTYDFVDPSTEQEEVNT 67
 QY 65 IAAPIDSAIQYNGTIFAYGQTASGKTYTMG-----SEDLGVIPRAIHDFOKIK 117
 DB 68 AVAPLKGVPKGNATVLAQGTGSKTYSMGAYTAQENEPVGVIPRVIQLLFKEID 127
 QY 118 KFPDREFLLRVSYMEIYNETITDLCGTQKMKPLIREDVNRNVVADLTTEEVTSEMA 177
 DB 128 KKSDFEFTLKVSYLEIYNEEILDLCPSREKAQINREDPKGKIVGLTEKTVLVALDT 187
 QY 178 LKWITKGEKSRHYGETKMNQSRSHITFRMILSRKGEPSNCEGSKVSHLNLVDLAG 237
 DB 188 VSCLEQGNNSRTVASTAMNSQSSRSHAFTI--SLEQKKSKDNSSPR-SKLHLVDLAG 243
 QY 238 SERAAQTGAAGVRLKEGNCINRSIFILGOVTKKLSGQVGFYNYRDSKLTRELQNSLGG 297
 DB 244 SERQKTKAEGDRKKEGININRGLLCLGNVISALGDDKGGFVYRDSKLTRELQNSLGG 303
 QY 298 NPKTRIICITTPV--SFDETLTALQFASTAK 326
 DB 304 NSHTLMIACVSPADSNLEETLNTLRYADRAR 334

RESULT 7

US-09-592-054-8
 ; Sequence 8, Application US/09592054
 ; Patent No. 6440684
 ; GENERAL INFORMATION:

; APPLICANT: Beraud, Christophe
 ; APPLICANT: Finer, Jeffrey
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Wood, Kenneth

TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
US-08-713-815A-4

Query Match 35.2%; Score 593.5; DB 2; Length 411;
Best Local Similarity 45.2%; Pred. No. 1.7e-54;
Matches 152; Conservative 42; Mismatches 119; Indels 23; Gaps 12;

QY 1 AEEGAVAVCVVRPLNSREESLGETAQVYKTDNNV---IYQVDGSKSFNFDVFGHNET 57
Db 9 AEDSIKVVVC-RRPLNDSEKAGSKFV--KFPNNVEENCISAG-KVILFDKVFKNAS 64
QY 58 TKNVYEIEAIPIDSAIQNGTIFAYGOTASCKTYTM---MGSEDLGLVPIRAIHDFQ 114
Db 65 QEKVYNEAAKSIYDVLGNGTIFAYGOTSSSKTHMEGVIGDSVKQGIIPRVNDIFN 124
QY 115 KIRKEP-DREFLLRVSYMEIYNETITDLCGTQRMKPLIREDVNRNYYVADLTFEEVYVT 173
Db 125 HIYAMEVNFELHFKVSYEIMDKIRDL--DVSKVN-LSVHEDKNRPVYVKGATERFVSS 182
QY 174 SEMALKWITKGEKSRHYGETQNRQSRSHITIFRMILESREKGEPSNCEGSKVYS-HNL 232
Db 183 PEDVFEVIEEGKNRHIATVNMNHSRSHSVFLNVKQ-----ENLENOKKLSGKLYL 236
QY 233 VDLAGSRAAQTGAAGVRLKEGNNRSLFILGOVIKKLSGQVGGFINYRDSKLTIRLQ 292
Db 237 VDLAGSEKVKTAGBTGLDEAKNINKLSALGNVISALADGN-KTHIPYRDSKLTIRLQ 295
QY 293 NSLGNPKTRIICTITPVSPD--ETLTALQFASAK 326
Db 296 ESLGNARTTIVICSPASNESETKSLDGFGRBK 331

RESULT 9
US-08-713-815A-3
Sequence 3, Application US/08713815A
Patent No. 5830659
GENERAL INFORMATION:
APPLICANT: Russell J. Stewart
TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
TITLE OF INVENTION: SEPARATIONS BY KINESINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
STREET: 9035 South 700 East, Suite 200
CITY: Sandy
STATE: Utah
COUNTRY: USA
ZIP: 84070
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: AST Ascentia 900N
OPERATING SYSTEM: DOS 6.22
SOFTWARE: Word Perfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,815A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. Howarth
REGISTRATION NUMBER: 36,553
REFERENCE/DOCKET NUMBER: T3214/U-2202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acid residues
TYPE: amino acid

TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
FILE REFERENCE: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1234
TYPE: PRT
ORGANISM: Human
US-09-592-054-8

Query Match 37.1%; Score 626; DB 4; Length 1234;
Best Local Similarity 43.5%; Pred. No. 3.3e-57;
Matches 144; Conservative 55; Mismatches 116; Indels 16; Gaps 6;

QY 6 VAVCVVRPLNSREESLG-ETAQVYKTDNNVIYQVDGSKSFNFDVFGHNETTKNYEE 64
Db 10 VRVALRCRPLVPKPEISRGCMCLSFVEGETQVVVGTD--KSFTYDFVDPCTQEEVFNK 67
QY 65 IAPIDSAIQNGTIFAYGOTASGKTYTMG-----SEDLGLVPIRAIHDFQIK 117
Db 68 AVAPLIGIKFGYNATVLAIGTQSGKTSYSGGAYTAEQENEPVGIIPRVILQFKRID 127
QY 118 KFPREFLLRVSYMEIYNETITDLCGTQRMKPLIREDVNRNYYVADLTFEEVYVTSEMA 177
Db 128 QKSDFEFTLVKSYLEIYNEEILDLCPREKAQINIREDPKEGIKIVGLTEKTVLVALDT 187
QY 178 LKWTKEKSRHYGETQNRQSRSHITIFRMILSREKGEPSNCEGSKVYSHLNLVDLAG 237
Db 188 VSCLEQGNNSRTVASTAMNSQSRSHAFIT--SLSGKKSKDNKNSFR-SKLHLVDLAG 243
QY 238 SERAAQTGAAGVRLKEGNNRSLFILGOVIKKLSGQVGGFINYRDSKLTIRLQNSLGG 297
Db 244 SEROKTKAEGDRLEKGINIRGLCLGNVISALGDDKKGSFVPRDSKLTIRLQDSLGG 303
QY 298 NPKTRIICTITPV--SPDETILALQFASAK 326
Db 304 NSHTLMIAVCVSPADSNLEETLSTLYADRAR 334

RESULT 8
US-08-713-815A-4
Sequence 4, Application US/08713815A
Patent No. 5830659
GENERAL INFORMATION:
APPLICANT: Russell J. Stewart
TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
TITLE OF INVENTION: SEPARATIONS BY KINESINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
STREET: 9035 South 700 East, Suite 200
CITY: Sandy
STATE: Utah
COUNTRY: USA
ZIP: 84070
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: AST Ascentia 900N
OPERATING SYSTEM: DOS 6.22
SOFTWARE: Word Perfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,815A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. Howarth
REGISTRATION NUMBER: 36,553
REFERENCE/DOCKET NUMBER: T3214/U-2202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633


```

; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Human
US-09-723-262-4

Query Match      35.1%; Score 592; DB 4; Length 375;
Best Local Similarity 43.1%; Pred. No. 2.1e-54;
Matches 153; Conservative 47; Mismatches 109; Indels 46; Gaps 10;

QY 2 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 49
Db 23 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 73

QY 50 RVFHGNETTKNVEEIAPIIDSAIQYNGTIFAYGQTASGKTYTMWG-----SEDHL 102
Db 74 HVADVDTTQESVFATVAKSIVESCMSGYNGTIFAYGQTASGKTYTMWGPFSDNFSHNL 133

QY 103 GVIPRAIHDIF-----QKIKKFPDRFLLRVSYMEIYNETITDLCGTQKMKPLIREDV 157
Db 134 GVIPRSEYLFSLIDREKEKAGAKSFLCKCSFIEIYNEQIYDLL--DSASAGLYLREHI 191

QY 158 NRNVYVADLTVEVYVTSSEMALKWITKGEKSRHYGETKMNORSSRSHHTIFRMILESREKGE 217
Db 192 KKGFFVVGAVEQVVTSAAEAYQVLGGWRNRVASTSMNRRSSRSHAVFTTIESMEK-- 249

QY 218 PSNCEGSKVSHNLNLDLAGSRAAQTGAAGVRLKEGCNINRSLFILGOVIKKLSGQVG 277
Db 250 -SNEIVNIRTSLLNLDLAGSERQKDTAEGMRLKEAGNINRSLCLGQVITLVD--VG 306

QY 278 G----FINYRDSKLTIRLQNSLGGNPKTRIICITTPVS--FDETITLQFASAK 326
Db 307 NGKQRHVCYRDSKLTFLRLDSLGNAKTAIIANVHPGRCFCGTSLTLNFAQRAK 361

RESULT 14
US-09-572-191-6
; Sequence 6, Application US/09572191
; Patent No. 6355466
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: No. 6355466el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1017
; CURRENT APPLICATION NUMBER: US/09/572,191
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Human
US-09-572-191-6

```

```

Query Match      35.1%; Score 592; DB 4; Length 409;
Best Local Similarity 43.1%; Pred. No. 2.4e-54;
Matches 153; Conservative 47; Mismatches 109; Indels 46; Gaps 10;

QY 2 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 49
Db 23 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 73

QY 50 RVFHGNETTKNVEEIAPIIDSAIQYNGTIFAYGQTASGKTYTMWG-----SEDHL 102
Db 74 HVADVDTTQESVFATVAKSIVESCMSGYNGTIFAYGQTASGKTYTMWGPFSDNFSHNL 133

QY 103 GVIPRAIHDIF-----QKIKKFPDRFLLRVSYMEIYNETITDLCGTQKMKPLIREDV 157
Db 134 GVIPRSEYLFSLIDREKEKAGAKSFLCKCSFIEIYNEQIYDLL--DSASAGLYLREHI 191

QY 158 NRNVYVADLTVEVYVTSSEMALKWITKGEKSRHYGETKMNORSSRSHHTIFRMILESREKGE 217
Db 192 KKGFFVVGAVEQVVTSAAEAYQVLGGWRNRVASTSMNRRSSRSHAVFTTIESMEK-- 249

QY 218 PSNCEGSKVSHNLNLDLAGSRAAQTGAAGVRLKEGCNINRSLFILGOVIKKLSGQVG 277
Db 250 -SNEIVNIRTSLLNLDLAGSERQKDTAEGMRLKEAGNINRSLCLGQVITLVD--VG 306

QY 278 G----FINYRDSKLTIRLQNSLGGNPKTRIICITTPVS--FDETITLQFASAK 326
Db 307 NGKQRHVCYRDSKLTFLRLDSLGNAKTAIIANVHPGRCFCGTSLTLNFAQRAK 361

RESULT 15
US-09-723-262-6
; Sequence 6, Application US/09723262
; Patent No. 6379912
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Sakowicz, Roman

```

```

; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Human
US-09-723-262-4

Query Match      35.1%; Score 592; DB 4; Length 375;
Best Local Similarity 43.1%; Pred. No. 2.1e-54;
Matches 153; Conservative 47; Mismatches 109; Indels 46; Gaps 10;

QY 2 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 49
Db 23 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 73

QY 50 RVFHGNETTKNVEEIAPIIDSAIQYNGTIFAYGQTASGKTYTMWG-----SEDHL 102
Db 74 HVADVDTTQESVFATVAKSIVESCMSGYNGTIFAYGQTASGKTYTMWGPFSDNFSHNL 133

QY 103 GVIPRAIHDIF-----QKIKKFPDRFLLRVSYMEIYNETITDLCGTQKMKPLIREDV 157
Db 134 GVIPRSEYLFSLIDREKEKAGAKSFLCKCSFIEIYNEQIYDLL--DSASAGLYLREHI 191

QY 158 NRNVYVADLTVEVYVTSSEMALKWITKGEKSRHYGETKMNORSSRSHHTIFRMILESREKGE 217
Db 192 KKGFFVVGAVEQVVTSAAEAYQVLGGWRNRVASTSMNRRSSRSHAVFTTIESMEK-- 249

QY 218 PSNCEGSKVSHNLNLDLAGSRAAQTGAAGVRLKEGCNINRSLFILGOVIKKLSGQVG 277
Db 250 -SNEIVNIRTSLLNLDLAGSERQKDTAEGMRLKEAGNINRSLCLGQVITLVD--VG 306

QY 278 G----FINYRDSKLTIRLQNSLGGNPKTRIICITTPVS--FDETITLQFASAK 326
Db 307 NGKQRHVCYRDSKLTFLRLDSLGNAKTAIIANVHPGRCFCGTSLTLNFAQRAK 361

RESULT 13
US-09-723-219-4
; Sequence 4, Application US/09723219
; Patent No. 6391613
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: No. 6391613el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1017
; CURRENT APPLICATION NUMBER: US/09/723,219
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/572,191
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Human
US-09-723-219-4

```

```

Query Match      35.1%; Score 592; DB 4; Length 375;
Best Local Similarity 43.1%; Pred. No. 2.1e-54;
Matches 153; Conservative 47; Mismatches 109; Indels 46; Gaps 10;

QY 2 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 49
Db 23 EGVAVVAVRVRPLNSREESL-GETAQVYWKTDNNVIYQVDS-----KSFNFD 73

QY 50 RVFHGNETTKNVEEIAPIIDSAIQYNGTIFAYGQTASGKTYTMWG-----SEDHL 102
Db 74 HVADVDTTQESVFATVAKSIVESCMSGYNGTIFAYGQTASGKTYTMWGPFSDNFSHNL 133

QY 103 GVIPRAIHDIF-----QKIKKFPDRFLLRVSYMEIYNETITDLCGTQKMKPLIREDV 157

```

```
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6379912el motor proteins and methods for
; FILE REFERENCE: 1017
; CURRENT APPLICATION NUMBER: US/09/723,262
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/572,191
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Human
US-09-723-262-6

Query Match      35.1%; Score 592; DB 4; Length 409;
Best Local Similarity 43.1%; Pred.No.2.4e-54;
Matches 153; Conservative 47; Mismatches 109; Indels 46; Gaps 10;

QY 2 EGAVAVCVVRPINSREESL-GETAQVYWKTDNNVIYQVDGS-----KSFNF 49
Db 23 EGDAIKVFVRIRPPAERSGADGE-----QNLCLSVLSSTSLHLHSNPEPKFTFD 73
QY 50 RVFHGNETTKNVYEETAAPIIDSAIOGYNGTIFAYGQTASGKTYTMWG-----SEDHL 102
Db 74 HVADVDTQESVFATVAKSIVESCMSGYNGTIFAYGQTSGKFTTWMGPSESDNFSHNL 133
QY 103 GVIPRAIHDF-----QKIKKFPDREFLLRVSYMEIYNETITDLCGTQWKPLIREDV 157
Db 134 GVIPRSFEYLFSLIDREKEKAGAGKSFCLKCSFIEIYNEQIYDLL--DSASAGLYLRHI 191
QY 158 NNNVYVADLTEVVYTSSEMALKWITKESRHYGETKMNQRSRSHITIFRMILESEKGE 217
Db 192 KKGVFVVGAVEQVWTSAAEAYQVLSGWRNRVASTMNRSSRSRSHAVFTIIESMEK-- 249
QY 218 PNCCEGSKVSHNLVLDLAGSRAAQTGAAGVRLKEGCNINRSLFLLGQVIKKLSDGQVG 277
Db 250 -SNEIVNKTSLNLVLDLAGSERQKDTAEGMRLKEAGNINRSLSLGQVITALVD--VG 306
QY 278 G----FINVRDSKLTRILONSLGGNPKTRIICTITPVS--FDETLTALOFASTAK 326
Db 307 NGKQRHVVCYRDSKLTFLELSDSLGGNAKTAIIANVHPGSRFCGETLSTLNFQRAK 361
```

Search completed: July 29, 2004, 09:42:44
Job time : 6.81089 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 09:39:47 ; Search time 16.3825 Seconds
(without alignments)

6280.361 Million cell updates/sec

Title: US-10-045-631B-88_COPY_2_329

Perfect score: 1686

Sequence: 1 AEEGAVAVCVRVPLNSREE.....PVSFDETLALQPASTAKYM 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	810.5	48.1	1382	16	US-10-437-963-176714
2	770.5	45.7	694	12	US-10-425-114-59725
3	664	33.4	1006	16	US-10-437-963-147933
4	651	38.6	956	16	US-10-437-963-182113
5	645.5	38.3	955	12	US-10-425-114-62672
6	643	38.1	1232	14	US-10-116-712-670
7	643	38.1	1232	15	US-10-408-765A-2153
8	643	38.1	1235	15	US-10-334-143-8
9	641.5	38.0	420	16	US-10-437-963-114373
10	638	37.8	1237	15	US-10-334-143-33
11	633	37.5	1232	14	US-10-116-712-664
12	633	37.5	1232	14	US-10-116-712-669
13	624.5	37.0	1029	16	US-10-311-642-2
14	620.5	36.8	1029	16	US-10-311-642-4
15	615.5	36.5	965	16	US-10-437-963-169150

16	612.5	36.3	966	12	US-10-425-114-62697	Sequence 62697, A
17	610	36.2	672	16	US-10-408-765A-1664	Sequence 1664, Ap
18	598.5	35.5	517	15	US-10-369-493-12881	Sequence 12881, A
19	593.5	35.2	975	14	US-10-080-608A-19	Sequence 19, Appl
20	593.5	35.2	975	15	US-10-370-685-108	Sequence 108, App
21	592	35.1	375	12	US-10-332-089-4	Sequence 4, Appl
22	592	35.1	409	12	US-10-332-089-6	Sequence 6, Appl
23	592	35.1	1388	12	US-10-332-089-2	Sequence 2, Appl
24	592	35.1	1388	14	US-10-146-473-82	Sequence 82, Appl
25	592	35.1	1388	15	US-10-173-999-32	Sequence 32, Appl
26	592	35.1	1388	16	US-10-188-832-164	Sequence 164, App
27	591.5	35.1	1031	14	US-10-080-608A-24	Sequence 24, Appl
28	591.5	35.1	1031	15	US-10-370-685-113	Sequence 113, App
29	588.5	34.9	757	12	US-10-220-120-366	Sequence 366, App
30	588.5	34.9	757	16	US-10-363-829-316	Sequence 316, App
31	588	34.9	406	15	US-10-369-493-3789	Sequence 3789, Ap
32	588	34.9	1045	16	US-10-437-963-150217	Sequence 150217, A
33	584	34.6	352	12	US-10-296-838-4	Sequence 4, Appl
34	584	34.6	1362	12	US-10-296-838-2	Sequence 2, Appl
35	583.5	34.6	2552	16	US-10-437-963-129734	Sequence 129734, A
36	583	34.6	963	14	US-10-080-608A-22	Sequence 22, Appl
37	583	34.6	963	15	US-10-370-685-111	Sequence 111, App
38	582	34.5	928	14	US-10-080-608A-23	Sequence 23, Appl
39	582	34.5	928	15	US-10-370-685-112	Sequence 112, App
40	582	34.5	963	14	US-10-080-608A-20	Sequence 20, Appl
41	582	34.5	963	15	US-10-370-685-109	Sequence 109, App
42	580.5	34.4	1011	12	US-10-336-472-24	Sequence 24, Appl
43	580.5	34.4	1011	12	US-10-236-417-58	Sequence 58, Appl
44	580.5	34.4	1032	14	US-10-080-608A-26	Sequence 26, Appl
45	580.5	34.4	1032	15	US-10-370-685-115	Sequence 115, App

ALIGNMENTS

RESULT 1

US-10-437-963-176714

; Sequence 176714, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 176714

; LENGTH: 1382

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_74437C.1.pep

US-10-437-963-176714

Query Match

Best Local Similarity 48.1%; Score 810.5; DB 16; Length 1382;

Matches 181; Conservative 43; Mismatches 88; Indels 17; Gaps 8;

Qy 6 VAVCVRVPLNSREESGETAQVYTWKTDNNVI-YQVDSKSFNDRVPHGNETTKNVYEE 64

Db 4 IHVAVRPLTA--EDAGSSP---WRVSGNAIALSTQPSIRFEFRIFGEERCRTADVGA 58

Qy 65 IAAPIIDSAIQVNGTIFAYGQTASGKTYMMGSEDLHGVIPRAIHDFIQIKKFPDEF 124

Db 59 RTKHIVDSAVRGNGTIFAYGQNSGKTYNRGSGNEFGIIPLAHDLFRTIEHLOREF 118

```
QY 125 LLKRVSYMEIYNETITDLGCTQKMKPLIREDVNRNVYVADLTEEVVYVSEMALKWITKG 184
Db 119 LRMSTWMEIYNEINDLL--VPEHRKLQIHESIERGLYVAGLREEIVTCPEQVLEFMSFG 176
QY 185 EKSRRHYGETKMNORSRSHITFRMILSRKGPSS-----NCEGSVKVSHNLVLDLAGSER 240
Db 177 ESHRHIGETNMNVYSRSHITFRMVIESREKVDSEAGESCD-AVRVSVNLVLDLAGSER 235
QY 241 AAGTGAAGVRLKEGCNINRSLFILGOVKKLSDG--QVGGFINVRDSKLTFRILQNSLGGN 298
Db 236 AAKTGAAGVRLKEGSHINKSLMTLGTIVKKLSGIEGQGHVYRDSKLTFRILQPALGNN 295
QY 299 PKTRIICTIT--PVSFDETLTALQFASTA 325
Db 296 ANTALICNITLAQVHADETKSLQFASRA 324

RESULT 2
US-10-425-114-59725
; Sequence 59725, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59725
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3912-011-C4_FLI.pep
US-10-425-114-59725

Query Match 45.7%; Score 770.5; DB 12; Length 694;
Best Local Similarity 50.1%; Pred. No. 2e-70;
Matches 168; Conservative 53; Mismatches 97; Indels 17; Gaps 7;

QY 6 VAVCVVRP-----LNSREESLGETAQVYWKTDN--NVIIYQVDG---SKSFNDRVFEHG 54
Db 30 ISVAVRFPNPLVAANTSPASGGGGDREWRIDTRVSLDLHRAAGPITGASFADHVFEG 89
QY 55 NETKNVYEEIAAPLIDSAIQYNGTIFAYGOTASGKTYTMMGSEDLHLGVIPRAIHDIFQ 114
Db 90 AANREIYGVTVREILGAVVGFGNGTAFAYGQTSKGTFMTNGSDADPGIIPRAVRVFD 149
QY 115 KIKFPDREFLRVSYMEIYNETITDLGCTQKMKPLIREDVNRNVYVADLTEEVVYTS 174
Db 150 TVRQADREFLRVSYMEIYNEINDLL--TLGQKLKTHESLDRGVYVSGUREIIVNSA 207
QY 175 ENALKWITKGEKSRHYGETKMNORSRSHITFRMILSRKGPSSNCEGSVKVSHNLVLD 234
Db 208 EQVFELLQGEANRHIFGETNMNRSRSHITFRMVIESRGKQDTGGD-AIRVSVNLVD 266
QY 235 LAGSFAAQTGAAGVRLKEGCNINRSLFILGOVKKLSD-QGVGGFINVRDSKLTFRILQ 293
Db 267 LAGSERIITGAEGVRLNEGKYNKSLMILGNVINKLSENGKQGRGHIPYRDSKLTFRILQ 326
QY 294 SLGGNPKTRIICTITP--VSFDETLTALQFASTAK 326
Db 327 ALGNNAKTSIICTAAPEEIHIEETRGTLQFASRAK 361

RESULT 3
```

```
US-10-437-963-147933
; Sequence 147933, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147933
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1006)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48414C.1.pep
US-10-437-963-147933

Query Match 39.4%; Score 664; DB 16; Length 1006;
Best Local Similarity 45.8%; Pred. No. 3.9e-59;
Matches 153; Conservative 62; Mismatches 105; Indels 14; Gaps 9;

QY 1 AEGAVAVCVVRPLNSREESLGETAQVYWKTDNNVIIYQVDGSK-SFNFDREVHGNETTK 59
Db 64 AAKESVAVVRFPPLSPREVRGE--KIAWYADGETVARSEQSNLAYAYDRVFGPTTTR 121
QY 60 NYVEEIAAPLIDSAIQYNGTIFAYGOTASGKTYTMMGSEDLHLGVIPRAIHDIFQIKKF 119
Db 122 HIYDAVAYVVGNGAMKNGITFAYGVTSKTKTHMGDQISPGVPLAVKDFINLIQET 181
QY 120 PDREFLRVSYMEIYNETITDLGCTQKMKPLIREDVNRNVYVADLTEEVVYVSEMALK 179
Db 182 PNREFLRVSYLEIYNEVNDLL--NPAQNLRIREDLQGTI--VEGIKEEAVLSPVHALS 238
QY 180 WITKGE---KSRHYGETKMNORSRSHITFRMILSRKGPSSNCEGSVKVSHNLVLDLA 236
Db 239 LIAAGEVFSELRHVGSTNFNLLSRSHITFTLTIESPRGGSNEAE-AVTLSQLNLIDLA 297
QY 237 GSRAAQTGAAGVRLKEGCNINRSLFILGOVKKLSDQGVGGFINVRDSKLTFRILQNSIG 296
Db 298 GSE--SSRVETAGVHQKEGYNKSLTLGKVISKLTID-EKATHIPFRDSKLTFRLLKSSLS 355
QY 297 GNPKTRIICTITPVS--FDETLTALQFASTAKYM 328
Db 356 GQGRVSLICTVTPASSNSEETHNTLKFAHRAKHI 389

RESULT 4
US-10-437-963-182113
; Sequence 182113, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
```

```
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 182113
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(956)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79331C.1.pap
; US-10-437-963-182113

Query Match
Best Local Similarity 38.6%; Score 651; DB 16; Length 956;
Matches 156; Conservative 51; Mismatches 106; Indels 22; Gaps 8;

QY 2 EGA VAVCVVRPLNSREESIGETAQVYWK--VIQVD-----GSKSENFDRVPHG 54
Db 31 KEEKIFVTVRPLSKKELAKO--QVWECDDNQITLYKGPDPDRAAPTSTYTFDKVFGP 88
QY 55 NETTKNVEEIAPIIDSALQGVNGTIPAYQOTASGKTYTMMGSEDLGVIPRAIHDF 114
Db 89 ASQTEVVEEGAKDVAMSALTGINATIFAYGQTSSGKTFTMR-----GVTESAVNDIYR 142
QY 115 KIKKFPDREFLLRVSVMEIYNETITDLCTQKMKPLIREDVNRNRYVADLTREVVYT 174
Db 143 HIENITPERFIIKISAMEIYNEIVKDLL--RPSTNLRLLDDPEKGTIVKLEEEIAKDS 200
QY 175 EMALKWITKGEKSRHYGETKMNQSRSHITFRMILESREKGPSPNCEGSKVYKSHLNLV 234
Db 201 QHLRHLISICEQORQVGETALNDTSSRSHQIILTLVESRLR-EVSGCVKSF-VANLNFV 258
QY 235 LAGSERAAGTGAAGVRLKEGCNINRSLFILGOVVKLSGQGVGFYINRDSKLTILQNS 294
Db 259 LAGSERAAGTGAAGVRLKEGCNINRSLLTITVIRKLSGKRSCHIPYRDSKLTILQNS 318
QY 295 LGGNPKTRIICTITPVSPF---DETLTALQFASTAK 326
Db 319 LGGNARTALICTMSPAQTHTVEQSRNTLFFATCAK 353

RESULT 5
US-10-425-114-62672
; Sequence 62672, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62672
; LENGTH: 955
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-241-All_FLI.pap
; US-10-425-114-62672

Query Match
Best Local Similarity 38.3%; Score 645.5; DB 12; Length 955;
Matches 156; Conservative 51; Mismatches 106; Indels 22; Gaps 8;

US-10-045-631b-88_copy_2_329.rapb
```

```
Matches 157; Conservative 45; Mismatches 112; Indels 21; Gaps 8;

QY 1 AEGAVAVCVVRPLNSREESIGETAQVYWK--TDNNVIYQVDGS-----KSENFDRVPH 53
Db 33 AKEEKIFVTVRPLSKKELAKO--QVWECDDNQITLYKGPDPDRAAPTSTYTFDKVFG 90
QY 54 GNETTKNVEEIAPIIDSALQGVNGTIPAYQOTASGKTYTMMGSEDLGVIPRAIHDF 113
Db 91 PACQTDVVVEEGAKDVAMSALTGINATIFAYGQTSSGKTFTMR-----GVTESAVNDIY 144
QY 114 QKIKKFPDREFLLRVSVMEIYNETITDLCTQKMKPLIREDVNRNRYVADLTREVVYT 173
Db 145 RHIDSTPERFIIKISAMEIYNEIVKDLL--RPDSAPLRLLDDPEKGTIVKLEEEIAK 202
QY 174 SEMALKWITKGEKSRHYGETKMNQSRSHITFRMILESREKGPSPNCEGSKVYKSHLNLV 233
Db 203 SQRHLRHLISICEQORQVGETALNDTSSRSHQIILTLVESRLR-EVSGCVKSF-VANLNFV 260
QY 234 DLGSERAAGTGAAGVRLKEGCNINRSLFILGOVVKLSGQGVGFYINRDSKLTILQNS 293
Db 261 DLGSERAAGTGAAGVRLKEGCNINRSLLTITVIRKLSGKRSCHIPYRDSKLTILQNS 320
QY 294 SLGNPKTRIICTITPVSPF---DETLTALQFASTAK 326
Db 321 SLGNARTALICTMSPAQTHTVEQSRNTLFFATCAK 353

RESULT 6
US-10-116-712-670
; Sequence 670, Application US/10116712
; Publication No. US2003019476A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-116-712-670

Query Match
Best Local Similarity 38.1%; Score 643; DB 14; Length 1232;
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;

QY 6 VAVCVVRPLNSREESIG-ETAQVYWKTDNNVIYQVDGSKSFNDRVPHGNETTKNVEE 64
Db 10 VRVALRCHPLVPKEITSEGCQMLSFVPGEPPQVVGTD--KSTYDFVDFDSTEQBEVNT 67
QY 65 IAAPIIDSALQGVNGTIPAYQOTASGKTYTMMG-----SEDLGVIPRAIHDFQKIK 117
Db 68 AVAPLKGKGVFGYNATVLAQGTGSGKTYSMGAVTAQEENEPTGVIPRVILQLLPEKD 127
QY 118 KFPDREFLLRVSVMEIYNETITDLCTQKMKPLIREDVNRNRYVADLTREVVYTSEMA 177
Db 128 KKSDFEFTLRVSYLEIYNEIYNEIYNEIYNEIYNEIYNEIYNEIYNEIYNEIYNEIY 187
QY 178 LKWKTKGEKSRHYGETKMNQSRSHITFRMILESREKGPSPNCEGSKVYKSHLNLV 237
Db 188 VSCLEQNNSTVASTAMNSQSSRSHAFITLSLQKRSKSD-----KNSFRSKLHLVDIAG 243
QY 238 SERAAQTGAAGVRLKEGCNINRSLFILGOVVKLSGQGVGFYINRDSKLTILQNSLGG 297
Db 244 SEROKTKAEGDRLKEGINNRGLCLGNVISALGDDKKGFGFYRDSKLTILQNSLGG 303
QY 298 NPKTRIICTITPVSPF---DETLTALQFASTAK 326
Db 321 NPKTRIICTITPVSPF---DETLTALQFASTAK 353
```

```
Db 304 NSHTLMIACVSPADSNLEETLNTLYRADRAR 334

; SEQ ID NO 8
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-8

Query Match 38.1%; Score 643; DB 15; Length 1235;
Best Local Similarity 44.4%; Pred. No. 8.e-57;
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;

QY 6 VAVCVVRPLNSREESLG-ETAQVYWKTDNNVYQVDSKSFNDFRVFHHGNETTKNVYEE 64
Db 13 VRVALRCRPLVPKEISEGCMCLSFVPGEPQVVVGTD--KSFTYDFVDFSTQEVEVT 70
QY 65 IAAPILDSAIQYNGTIFAYGQTASGKTYTMMG-----SEHGLGVIPRAIHDFQKIK 117
Db 71 AVAPLIKGVFKGNATVLAQGTSKTYSMGAYTAEQENETPTGVIPRVQLLFKEID 130
QY 118 KFPDRFLLRVSYMEIYNETITDLCGTQKMKPLIIREDVNRNVYVADLTREVVYTSMA 177
Db 131 KXSDFEFTLVSYLEIYNEEILDLLCPREKAQINIREDPKGIKIVGLTEKTVLVALDT 190
QY 178 LKWIITKGEKSRHYGETKMNORSRSHITFRMILSREKGPSPNCEGSKVSHNLVLDLAG 237
Db 191 VSCLEQGNNSRIVASTAMNSQSRSHAIPTISLEQRKKSD----KNSSFRSKLHLVLDLAG 246
QY 238 SERAAQTGAAGVRLKEGCNINRSLFILGOVIKKLSDGOVGGFVINYRDSKLTILQNSLGG 297
Db 247 SERQKTKAEGDRLKEGININRGLCLGNVISALGDDKKGFPVPRDSKLTILQNSLGG 306
QY 298 NPKTRIICITPV--SFDETLTALOPASTAK 326
Db 307 NSHTLMIACVSPADSNLEETLNTLYRADRAR 337

RESULT 9
US-10-437-963-114373
; Sequence 114373, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114373
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18070C.1.pep
US-10-437-963-114373

Query Match 38.0%; Score 641.5; DB 16; Length 420;
Best Local Similarity 44.1%; Pred. No. 2.2e-57;
Matches 146; Conservative 56; Mismatches 108; Indels 21; Gaps 6;

QY 6 VAVCVVRPLNSREESLG-ETAQVYWKTDNNVYQVDSKSFNDFRVFHHGNETTKNVYEE 57
Db 17 IVSVVRLRPVNAREERGDS--WECAGTTLITFRGAVPERAMFPASYSYDRVFSHECG 74
QY 58 TKNVYBEIAPIIDSATIQGYNGTIFAYGQTASGKTYTMMGSEHGLGVIPRAIHDFQKIK 117
Db 75 TRQVYDEGARQVAMSVLSGINASIFAYGQTSSGKTYTMMGITEY-----SMSDIYDYE 128

Db 304 NSHTLMIACVSPADSNLEETLNTLYRADRAR 334

; SEQ ID NO 8
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-8

Query Match 38.1%; Score 643; DB 16; Length 1232;
Best Local Similarity 44.4%; Pred. No. 8e-57;
Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;

QY 6 VAVCVVRPLNSREESLG-ETAQVYWKTDNNVYQVDSKSFNDFRVFHHGNETTKNVYEE 64
Db 10 VRVALRCRPLVPKEISEGCMCLSFVPGEPQVVVGTD--KSFTYDFVDFSTQEVEVT 67
QY 65 IAAPILDSAIQYNGTIFAYGQTASGKTYTMMG-----SEHGLGVIPRAIHDFQKIK 117
Db 68 AVAPLIKGVFKGNATVLAQGTSKTYSMGAYTAEQENETPTGVIPRVQLLFKEID 127
QY 118 KFPDRFLLRVSYMEIYNETITDLCGTQKMKPLIIREDVNRNVYVADLTREVVYTSMA 177
Db 128 KXSDFEFTLVSYLEIYNEEILDLLCPREKAQINIREDPKGIKIVGLTEKTVLVALDT 187
QY 178 LKWIITKGEKSRHYGETKMNORSRSHITFRMILSREKGPSPNCEGSKVSHNLVLDLAG 237
Db 188 VSCLEQGNNSRIVASTAMNSQSRSHAIPTISLEQRKKSD----KNSSFRSKLHLVLDLAG 243
QY 238 SERAAQTGAAGVRLKEGCNINRSLFILGOVIKKLSDGOVGGFVINYRDSKLTILQNSLGG 297
Db 244 SERQKTKAEGDRLKEGININRGLCLGNVISALGDDKKGFPVPRDSKLTILQNSLGG 303
QY 298 NPKTRIICITPV--SFDETLTALOPASTAK 326
Db 304 NSHTLMIACVSPADSNLEETLNTLYRADRAR 334

RESULT 8
US-10-334-143-8
; Sequence 8, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
```


[illegible]

Query Match	37.8%;	Score 638;	DB 15;	Length 1237;
Best Local Similarity	43.8%;	Pred. No. 2,7e-56;		
Matches 145;	Conservative 53;	Mismatches 117;	Indels 16;	Gaps 6;
QY	6	VAVCVRVRLNPSREESLG-ETAQVYWKTDNNVYQVDGSGKSPNDFRVFHGNETTKNVYEE	64	
dbb	13	VRVALRCRLPVEIKREISGQCMCLSPFVGETQVVVGTD--KSFTYDFVDFDCTQEVEFNK	70	
QY	65	IAAPILDSIAQGYNGTIFAYGQTASGKTYMMG-----SEDLGVIPRAIHDIQKIK	117	
dbb	71	AVAPLIKGFKNATVLAYQGTGSKTYSMGAYTABQENETFGIIRVIOQLLFKEID	130	
QY	118	KPFDREFLLRVSYMEIYNTITDLLCGTKMKPLIIREDVNRNVYVADITEVVYVSEMA	177	
dbb	131	KKSDPEFTLKVSLEYEINEEIIDLCPSEKKAQINREDPKEGIKIVGLTEKTVLVALDT	190	
QY	178	LKWITPKGEKSRHYGTQWQRSSRSHITIFRMILESEXKEGEPNCEGSKVSHNLNVDLAG	237	
dbb	191	VSCLEQGNNSRTVASTAMNSQSRSHAFTISIBQRKKSD-KNCSPR---SKLHLVDLAG	246	
QY	238	SERAAQTGAAGVRLKEGCNINRSLFTLGOVINKLSDGVGGGFINVRDSKLTRLILNSLGG	297	
dbb	247	SERQKTKAEGDRLKEGININRGLLCLGNVISAIGDDKKGSFVYRDSKLTRLLOQSLGG	306	
QY	298	NPKTEILCTITPV--SFDETTLALQFASTAK	326	
dbb	307	NSHTLMIAICVPADSNLEETLSTLRYADRAR	337	

```

; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 664
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-116-712-664

```

Accession	147	Conservative	51	Mismatches	117	Indels	16	Gaps	6
QY	6	VAYCVRVRLPKEEELIG-ETAQVYWKTDNNVLYQVDGSKSFNDFRVPHGNETTKNVYEE	64						
Db	10	VRVALACRLVPKELISEGQCLMSFGPBPQVVVGTD--KSFTYDFDFDSDTBOEYFNT	67						

Db 296 LQDSLGGTKILMWACLSPADNNYDETSLRYANRAK 333

RESULT 14

US-10-311-642-4

; Sequence 4, Application US/10311642

; Publication No. US20040086878A1

; GENERAL INFORMATION:

; APPLICANT: Cytokinetics, Inc.

; APPLICANT: Beraud, Christophe

; APPLICANT: Freedman, Richard

; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR

; FILE REFERENCE: 020552-001910US

; CURRENT APPLICATION NUMBER: US/10/311,642

; CURRENT FILING DATE: 2003-09-29

; PRIOR APPLICATION NUMBER: 09/597,602

; PRIOR FILING DATE: 2000-06-20

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence of preferred fragment of motor

; OTHER INFORMATION: domain of Hskif17.

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Hskif17

US-10-311-642-4

Query Match 36.8%; Score 620.5; DB 16; Length 329;

Best Local Similarity 42.7%; Pred. No. 2.2e-55;

Matches 144; Conservative 54; Mismatches 114; Indels 25; Gaps 8;

QY 6 VAVCVVRPLNSREESLGETAQVYWKTD-----NNVIYQVDGSKSFNDRVPHGNET 57

Db 1 KVIVVRCRPMQREEL--RCQPVTVVDCARAQCCIQNGGADEPPKQFTFDGAVHVDH 58

QY 58 TKNVVEETAAPIIDSAIQGYNGTIFAYGQTASGKTYTMGSED---HLGVIPRAIHDFQ 114

Db 59 TEQIYNEIAYPLVEGVTEGYNGTIFAYGQTSGKSFQMGLPDPSPQRGIIPRAFEHVF 118

QY 115 KIKKPPDFEFLRVSYMEIYNETITDLCGQTKMKPLIREDVNVNVAADLTSEWVYTS 174

Db 119 SVQCAENTKFLVRASYLEIYNEVDRLDGADTKQK-LELKEHPEKGVYVKGLSMHTVHS 177

QY 175 EMALKWITKGEKSRHVGTEKMNORSRSHITFPMILESR---EKGEPSNCEGSKVSHL 231

Db 178 AQCEHIMETGKNRSVGYTLNMKDSRSHSIFTISIEMSAVDERG-----KDLRAGKL 232

QY 232 LVDLAGSRAAQTGAAGVRLKEGCNINRSLFILGVIKLSQGVGGFNYNDRSKLTRIL 291

Db 233 LVDLAGSERQSKTGATGERLKEATKINLSLALGNVISALVDGRC-KHVPYRDSKLTRLL 291

QY 292 QNSLGNPKTRIICTITPV--SFDETLTAQFASTAK 326

Db 292 QDSLGGTKILMWACLSPADNNYDETSLRYANRAK 328

RESULT 15

US-10-437-963-169150

; Sequence 169150, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

QY 65 IAAPIDSAIQGYNGTIFAYGQTASGKTYTMG-----SEHLGVIPRAIHDFQKIK 117

Db 69 AVAPLIKGVKGNATVLAAYGQTSGKTYSMGAYTAEGENPTGVIPRVQLLPKEID 127

QY 118 KFPDFEFLRVSYMEIYNETITDLCGQTKMKPLIREDVNVNVAADLTSEWVYTS 177

Db 128 KXSDPEFTLKVSYLEINBEILDLCPREKAQINREDPKGEIKIVGLTEKTVLVALDT 187

QY 178 LWITKGEKSRHVGTEKMNORSRSHITFPMILESRKESKPSNCEGSKVSHLNLVDLAG 237

Db 188 VSLQEGNNSRTVASTAMNSQSRSHAFTI---SLEQKSKDNSSFR-SKLHLVDLAG 243

QY 238 SERAAQTGAAGVRLKEGCNINRSLFILGVIKLSQGVGGFNYNDRSKLTRILQNSLGG 297

Db 244 SEQOKTKAEDRLKEGININRGLCLGNVISALGDDKGGFAPYRDSKLTRILQNSLGG 303

QY 298 NPKTRIICTITPV--SFDETLTAQFASTAK 326

Db 304 NSHTLMIACVSPADSNLEETLNTLRYADRAR 334

RESULT 13

US-10-311-642-2

; Sequence 2, Application US/10311642

; Publication No. US20040086878A1

; GENERAL INFORMATION:

; APPLICANT: Cytokinetics, Inc.

; APPLICANT: Beraud, Christophe

; APPLICANT: Freedman, Richard

; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR

; FILE REFERENCE: 020552-001910US

; CURRENT APPLICATION NUMBER: US/10/311,642

; CURRENT FILING DATE: 2003-09-29

; PRIOR APPLICATION NUMBER: 09/597,602

; PRIOR FILING DATE: 2000-06-20

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1029

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Hskif17 amino acid sequence

; OTHER INFORMATION: Description of Artificial Sequence: Hskif17

US-10-311-642-2

Query Match 37.0%; Score 624.5; DB 16; Length 1029;

Best Local Similarity 42.9%; Pred. No. 5e-55;

Matches 145; Conservative 54; Mismatches 114; Indels 25; Gaps 8;

QY 5 AVAVCVVRPLNSREESLGETAQVYWKTD-----NNVIYQVDGSKSFNDRVPHGNE 56

Db 5 AVKVVRCRPMQREEL--RCQPVTVVDCARAQCCIQNGGADEPPKQFTFDGAVHVDH 62

QY 57 TKNVVEETAAPIIDSAIQGYNGTIFAYGQTASGKTYTMGSED---HLGVIPRAIHDF 113

Db 63 VTEQIYNEIAYPLVEGVTEGYNGTIFAYGQTSGKSFQMGLPDPSPQRGIIPRAFEHVF 122

QY 114 QIKKPPDFEFLRVSYMEIYNETITDLCGQTKMKPLIREDVNVNVAADLTSEWVYTS 173

Db 123 ESQCAENTKFLVRASYLEIYNEVDRLDGADTKQK-LELKEHPEKGVYVKGLSMHTVHS 181

QY 174 SEMALKWITKGEKSRHVGTEKMNORSRSHITFPMILESR---EKGEPSNCEGSKVSHL 230

Db 182 VAQCEHIMETGKNRSVGYTLNMKDSRSHSIFTISIEMSAVDERG-----KDLRAGKL 236

QY 231 NLVDLAGSRAAQTGAAGVRLKEGCNINRSLFILGVIKLSQGVGGFNYNDRSKLTRI 290

Db 237 NLVDLAGSERQSKTGATGERLKEATKINLSLALGNVISALVDGRC-KHVPYRDSKLTRL 295

QY 291 LQNSLGNPKTRIICTITPV--SFDETLTAQFASTAK 326

Query Match	36.5%;	Score	615.5;	DB	16;	Length	965;
Best Local Similarity	43.0%;	Pred.	No. 3.9e-54;				
Matches	144;	Conservative	52;	Mismatches	96;	Indels	43;
Gaps	7;						

QY	1	AEEGAVACVVRVRLPSRE-----ESLGETAQVTKTNNVIYQVDSKSNFDRVPH	53
Db	17	AKERIMVSVRLPLNGREGAGSDCECISPTTWMFRST--VPERAMFETAYTVDRVFG	73
QY	54	GNETTKNVYBEIAAPIIDSAAIQCYNGTIPAYGQTASGKVTYMMGSDHDLGVIPRAIHDIF	113
Db	74	PDSSTRQVYEEGAEKVALSVVSGINSIFAYGQTSKGKYYTMTGITET:::	127
QY	114	QTKKPFDFEFLRVSIMEIYNETITDLCGTOKMKPLIREDVNRNVVADLTEWVYT	173
Db	128	DYAEKPEREFILRFAEIYNEAVDDL--SHDTTPLRLDDPEKGTIVKLTETLSD	185
QY	174	SEMALKWITGKGRHYGTOMQRSRSHTFRMILESKGEPNCEGSKGVKSHNIV	233
Db	186	KOHLRNLLVCAQRQIGETALNETSRSHQILR-----LNPF	223
QY	234	DIAGERAQAQTGAAGVRLKEGCNINRSLFGLGVIKKLDGQGVGGFINVRDGLKLTILQN	293
Db	224	DLAGERASQTASAGVRLKEGSHINESLTLGKVVQQLSKGR-NGHIPYRDSKLTRLOS	282
QY	294	SIGGNPKTILICTIPV--SFDETLTALQFATAK	326
Db	283	SUGGNARTAILICTNGPASHIEQSRTNLLFATCAK	317

Search completed: July 29, 2004, 10:06:25
Job time : 17.3825 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 09:28:21 ; Search time 4.90075 Seconds
(without alignments)
6437.961 Million cell updates/sec

Title: US-10-045-631B-88_COPY_2_329
Perfect score: 1686
Sequence: 1 AEGGAVAVCVRPPLNSREE.....PVSFDETLTALQFASTAKYM 328

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1686	100.0	2663	1	S28261
2	1258.5	74.6	2354	2	T14156
3	773.5	45.9	823	2	T52425
4	738	43.8	888	2	D96619
5	663.5	39.4	1459	2	T30196
6	650	38.6	786	2	A53939
7	643	38.1	701	1	B44259
8	642	38.1	742	1	S58691
9	641.5	38.0	1231	2	A54803
10	630.5	37.4	909	2	H86350
11	630	37.4	747	1	A57107
12	628.5	37.3	1226	2	I51617
13	623.5	37.0	699	1	S38982
14	621	36.8	932	2	T49235
15	618.5	36.7	1121	2	T06065
16	612.5	36.3	968	2	T45746
17	608	36.1	1225	2	A56514
18	607	36.0	581	2	F84599
19	605	35.9	672	2	S54331
20	601.5	35.7	1263	2	T13465
21	597	35.4	332	2	C48895
22	595	35.3	1921	1	T13827
23	593.5	35.2	975	1	A31497
24	591.5	35.1	1031	1	A38713
25	591.5	35.1	1584	1	JN0114
26	591.5	35.1	1584	2	T15822
27	586.5	34.8	554	2	T50118
28	586	34.8	1254	2	T18277
29	585	34.7	793	2	JC5831

30 585 34.7 1076 2 B84687 probable kinesin-l
31 584.5 34.7 1130 2 T21134 hypothetical prote
32 582 34.5 928 2 T10164 kinesin heavy chai
33 582 34.5 963 1 A41919 kinesin heavy chai
34 582 34.5 1066 1 A48669 kinesin-related pr
35 580.5 34.4 1032 2 T38510 neuronal kinesin h
36 579.5 34.4 1388 2 T30335 KLP2 protein - Afr
37 579 34.3 968 2 T51933 kinesin motor prot
38 578.5 34.3 294 2 S38983 kinesin-related pr
39 576.5 34.2 967 1 A35075 kinesin heavy chai
40 573.5 34.0 1576 2 T29237 hypothetical prote
41 573 34.0 1027 2 S37711 kinesin heavy chai
42 572.5 34.0 834 2 T06055 hypothetical prote
43 571.5 33.9 935 2 T51930 kinesin (imported)
44 569 33.7 843 2 S44868 kinesin heavy chai
45 568 33.7 784 1 A55236 kinesin-related pr

ALIGNMENTS

RESULT 1
S28261

centromere protein E - human

N;Alternate names: Centromere 312K protein; kinesin-related protein CENP-E

C;Species: Homo sapiens (man)

C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001

C;Accession: S28261

R;Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.

Nature 359, 536-539, 1992

A;Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.

A;Reference number: S28261; MUID:93024922; PMID:1406971

A;Accession: S28261

A;Molecule type: mRNA

A;Residues: 1-2663 <YEN>

A;Cross-references: EMBL:Z15005; NID:G29864; PIDN:CAA78727.1; PID:G29865

C;Genetics:

A;Gene: GDB:CENPE

A;Cross-references: GDB:361164; OMIM:117143

A;Map position: 4q24-4q25

C;Superfamily: centromere protein E; kinesin motor domain homology

C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; P-loop

F;7-335/Domain: kinesin motor domain homology <KNOT>

F;86-93/Region: nucleotide-binding motif A (P-loop)

F;486-2183/Domain: coiled coil #status predicted <COI>

F;92/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 1686; DB 1; Length 2663;
Best Local Similarity 100.0%; Pred. No. 3.1e-120;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEGGAVAVCVRPPLNSREEISLGETAQVYWKTDNNVIYQVDSKSFNDRVPHGNETTKN 60

Db 2 AEGGAVAVCVRPPLNSREEISLGETAQVYWKTDNNVIYQVDSKSFNDRVPHGNETTKN 61

QY 61 VYEIIAIPIDSAIQGNGTIFAYGTASGKTYTMGSEDLGVIPRAIHDI FOKIKKFP 120

Db 62 VYEIIAIPIDSAIQGNGTIFAYGTASGKTYTMGSEDLGVIPRAIHDI FOKIKKFP 121

QY 121 DREPLLKVSMEIYNETITDLCGTQKMKPLIREDVNRNRYVADLTVEVVYTSMAALKW 180

Db 122 DREPLLKVSMEIYNETITDLCGTQKMKPLIREDVNRNRYVADLTVEVVYTSMAALKW 181

QY 181 ITKGESRRHYGETKMNQSSRSHTIFRMILESREKGPSPCEGSKVSHLNLDLAGSER 240

Db 182 ITKGESRRHYGETKMNQSSRSHTIFRMILESREKGPSPCEGSKVSHLNLDLAGSER 241

QY 241 AAGTGAAGVRLKEGCNINRSLFILGQVVKLSDGQVGGFINYRDSKLTILQNSLGNPK 300

Db 242 AAGTGAAGVRLKEGCNINRSLFILGQVVKLSDGQVGGFINYRDSKLTILQNSLGNPK 301

QY 301 TRIICITTPVSFDETLTALQFASTAKYM 328

Db 302 TRIICITIPVSEDTLTALQFASAKYM 329

RESULT 2

T14156

kinesin-related protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: T14156

R:Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.

Cell 91, 357-366, 1997

A:Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome

A:Reference number: Z17893; PMID:98028574; PMID:9363944

A:Accession: T14156

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2954 <WOO>

A:Cross-references: EMBL:AF027728; NID:g2586070; PID:g2586071; PIDN:AAC603C0.1

C:Genetics:

A:Gene: XCENP-E

C:Superfamily: centromere protein E; kinesin motor domain homology

Query Match 74.6%; Score 1258.5; DB 2; Length 2954;

Best Local Similarity 73.4%; Pred. No. 1.8e-87;

Matches 243; Conservative 40; Mismatches 43; Indels 5; Gaps 2;

QY 1 AEEGAVAVCVVRPLNSRERSLGETAQVYKTKDNNVIYQVDGSKSFN 60

Db 2 SEGDAVAVCVVRPLNIOREQ--GQANLQWAGNNTISQVDGTSKSFNDRVFNHSHSTQ 59

QY 61 VYEBIAAPIIDSAIQGYNGTIFAYGOTASGKTYTMMGSEDLGVIPRAIHDFOKIKKFP 120

Db 60 IYQEIAPILRSALQGYNGTIFAYGOTSSGKTYTMMGTPNSLGIPIQAIQEVFKIIQEP 119

QY 121 DREFLLRVSYMEIYNEITDLCGTQKMKPLIREDVNRNYYVADLTEEVVYTSSEMALKW 180

Db 120 NREFLLRVSYMEIYNETVKDLCDDRKKPLIEIDFNFNYYVADLTEELVWVPEHVIQW 179

QY 181 ITKGEKSRHYGETKNNQSSRSHTIFRMILSRKGEPS---NCEGSKVVKSHLNLVDLAG 237

Db 180 IKKGEKSRHYGETKNNHSSRSHTIFRMIVESDRNDPTNGENCDCGAVWVSHLNLVDLAG 239

QY 238 SERAAQTGAAGVRLKEGNCINRSLFILQGVIKKLSGQGVGFNNVRSKLTIRLQNSLGG 297

Db 240 SERASQTGAEGVRLKEGNCINRSLFILQGVIKKLSGQGVGFNNVRSKLTIRLQNSLGG 299

QY 298 NPKTRIICTITPVSFDTLTALQFASAKYM 328

Db 300 NAKTVIICITIPVSFDTLTSLTQFASAKHV 330

Query Match 43.8%; Score 738; DB 2; Length 888;

Best Local Similarity 46.4%; Pred. No. 2.3e-48;

Matches 173; Conservative 46; Mismatches 92; Indels 62; Gaps 8;

QY 6 VAVCVVRPLNSRERSLGETAQVYKTKDNNVIYQVDGSKSFN-----FDRVPHGNE 56

Db 4 ICVAVVRP-----PAPENGASLWKVEDN--RISLHKSLDTPITTASHAFDFVDESS 54

QY 57 TTKNVYEBIAAPIIDSAIQGYNGTIFAYGOTASGKTYTMMGSEDLGVIPRAIHDFOKI 116

Db 55 TNASVVELLTQDIIHAAVEGFNGTAFAYGOTSSGKTYTMMGSETDFTIERSVRDVERI 114

QY 117 KFPDREFLLRVSYMEIYNETTDLCLCGTQKMKPLIREDVNRNYYVADLTEEVVYTSSEM 176

Db 115 HMSDREFLLRVSYMEIYNEEINDLL--AVENQRLQIHEHLRGVFAVLKEEIVSDAEQ 172

QY 177 ALKWTITKGEKSRHYGETKNNQSSRSHTIFRMILSRKGEPSNCEGSKVVKSHLNLVDLA 236

Db 173 ILKLDSGEVNRHFGTNNVHSSRSHTIFRMVIESR--GKONSSSDAIRKSVNLNVDLA 230

QY 237 GSERAAQTGAAGVRLKEGNCINRSLFILQGVIKKLSGQGVGFNNVRSKLTIRLQNSL 295

Db 231 GSERIAKTGAGGVRLQEGKYINKSLMLGLNVINKLSDSYKLAHIFPYRDSKLTIRLQPAL 290

QY 296 GGNPKTRIICTITPVS--FDETLTALQFASAK 326

Db 291 GGNAKTIICTIAPPEHHIEESKGTLOFASRAK 323

RESULT 4

D96619

protein T30E16.9 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: D96619

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D96619

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-888 <STO>

A:Cross-references: GB:AE005173; NID:g8778739; PIDN:AAF79747.1; GSPDB:GN00141

C:Genetics:

A:Gene: T30E16.9

A:Map position: 1

Query Match 43.8%; Score 738; DB 2; Length 888;

Best Local Similarity 46.4%; Pred. No. 2.3e-48;

Matches 173; Conservative 46; Mismatches 92; Indels 62; Gaps 8;

QY 6 VAVCVVRPLNSRERSLGETAQVYKTKDNNVI-----FDRVPHGNE 56

Db 4 ICVAVVRP-----PAPENGASLWKVEDN--RISLHKSLDTPITTASHAFVSGISISTDLI 57

QY 39 QVDGSKSFN-----DRVFHGNETTNNVYEBIAAPIIDSAIQGYNGTIFAYGQTA 88

Db 58 EIVSLFLFSFVVYVFFLFDHVPFESSNVSVELLTKDIIHAAVEGFNGTAFAYGQTS 117

QY 89 SGKTYTMMGSEDLGVIPRAIHDFOKIKKFPDREFLLRVSYMEIYNEITDLCGTQXM 148

Db 118 SGKTYTMMGSETDPIIRSRVDRVFERIHMISDREFLLRVSYMEIYNEEINDLL--AVEN 175

QY 149 KPLIREDVNRNYYVADLTEEVVYSEMAKWTITKGEKSRHYGETKNNQSSRSHTIFRM 208

Db 176 QRLQIHEHLRGVFAVLKEEIVSDAEQILKLDSGEVNRHFGTNNVHSSRSHTIFRM 235

QY 209 -----TLESREKGEPSNCEGSKVVKSHLNLVDLAGSRAQTGAAGVRLKEGNCN 256

Db 236 VRFRSYERDILLVIESR--GKDNSSDAIRVSVNLVLDLAGSERIAKTGAGGVRLQEGKY 293
 QY 257 INRSILFQGVKKLSGQ-QVGGFNYRDSKLTILQNSLGNPKTRIICTITPVSV--FD 313
 Db 294 INKSLMILGNVINKLSDSSTKLRAHPYEDSKLTILQPALGNKATCIICIAPEEHIE 353
 QY 314 ETLTALQFASAK 326
 Db 354 ESKGTLOFASRAK 366

RESULT 5

T30196
 C:Species: Ustilago maydis (corn smut)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
 C:Accession: T30196
 R:Lehmler, C.; Steinberg, G.; Snetsetlaar, K.M.; Schliwa, M.; Kahmann, R.; Bolker, M.
 EMBL J. 16, 3464-3473, 1997
 A:Title: Identification of a motor protein required for filamentous growth in Ustilago
 A:Reference number: Z20770; MUID:97361828; PMID:9218789
 A:Accession: T30196
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1459 <LEH>
 A:Cross-references: EMBL:U92844; NID:g2062749; PID:g2062750; PIDN:AAB63336.1
 C:Genetics:
 A:Gene: kinl
 C:Function:
 A:Description: required for filamentous growth in Ustilago maydis

Query Match 39.4%; Score 663.5; DB 2; Length 1459;
 Best Local Similarity 39.8%; Pred. No. 2.2e-42;
 Matches 159; Conservative 51; Mismatches 100; Indels 89; Gaps 10;
 QY 6 VAVCVVRPLNSRREESLGTATQVYKTDN--NVIYQD----- 41
 Db 237 VVCFVMRP--SRASSDSEASV--MNCDSERKRIPTTEHPHAIKATKTTSSERAGASTA 293
 QY 42 -----GSKSFNDRVPHGNETTKNYYEETAAPILDSALIOGYNGTIFAYCQ 86
 Db 294 AAPSSHDLDHEDPTSTYHFQDKLITGAQTDDMTSHIAPVRAAVEGYNGTIFAYCQ 353
 QY 87 TASGTYTMMGSEDLGVIPRAIHIFQIKFKPPDPREFLLRVSYMEIYNETITDILCGTQ 146
 Db 354 TGSQKTHTMGSDAEFGVIPRAVEQIFQMIKDPREFLLRVSYMEIYNETILKLLA--- 410
 QY 147 KMKPL-----IREDVNRNYYVADLTTEVV 171
 Db 411 PLPPLTGTGSLQTTDRPASPIKGGSSHAQSQSCTLRIETDQKSRVITGLREIV 470
 QY 172 YTSEMALKWITKGEKSRHYGETKMNQSRSHHTIFRMILESEKGEPSNCGSVKVSIN 231
 Db 471 TDANTVLQIQGDERHVGTADWNERSSRCHVFQLIERSPAPSASKE--VRISQIN 528
 QY 232 LVDLAGSRAAQTGAAGVRLKEGCNINSLFILQGVIKKLSGQVGG--FINYRDSKLTR 289
 Db 529 LIDLAGSRAA---SQAEERKEGAFINKSLTLGTVICLTPVENGDAHPYRDSKLTR 585
 QY 290 ILQNSLGNPKTRIICTITPVSV--FDETLTALQFASAK 326
 Db 586 ILQTSLSGNARIIVICTLSPDTEHANEITLTKFGKCK 624

RESULT 6

A53939
 C:Species: Chlamydomonas reinhardtii
 C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001
 C:Accession: A53939
 R:Walther, Z.; Vashishtha, M.; Hall, J.L.
 J. Cell Biol. 126, 175-188, 1994
 A:Title: The Chlamydomonas FLA10 gene encodes a novel kinesin-homologous protein.

A:Reference number: A53939; MUID:94299638; PMID:8027176
 A:Accession: A53939
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-786 <WAL>
 A:Cross-references: EMBL:L33697; NID:g497696; PIDN:AAA21738.1; PID:g497697
 A:Note: authors translated the codon AAC for residue 753 as Asp
 C:Genetics:
 A:Gene: FLA10
 C:Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
 C:Keywords: ATP; coiled coil; nucleotide binding; P-loop
 F:11-359/Domain: kinesin motor domain homology <KMT>
 F:97-104/Region: nucleotide-binding motif A (P-loop)

Query Match 38.6%; Score 650; DB 2; Length 786;
 Best Local Similarity 44.8%; Pred. No. 1e-41;
 Matches 154; Conservative 56; Mismatches 110; Indels 24; Gaps 8;
 QY 5 AVAVCVVRPLNSRERSLGTATQVYKTDNNVIY----QVDSG---KSFNDRVFGHNET 57
 Db 10 SVKVVRCPLNGKEKADGRSIRVDMVDAGQVKVRNPKADASEPPKAFQDQVYDWNQC 69
 QY 58 TKNVYEEIAAPIIDSALIOGYNGTIFAYGQTASCTVTMMGSEDH---LGVIPRAIHIFQ 114
 Db 70 QRDVFDITARPLIDSCIEGYNGTIFAYGQTGKSHMEKGPPELRLGLIPTFRYVFE 129
 QY 115 KI--KKFPDREFLLRVSYMEIYNETITDILCGTQKMKPLIIREDVNRNYYVADLTTEVVYT 173
 Db 130 IIAKDSGTKEFLVRSYLYEINVEEDLL--GKDHKKMKELKESPDGRGVYVKDLSQFVCKN 188
 QY 174 SEMALKWITKGEKSRHYGETKMNQSRSHHTIFRMILESEK-----GEPSNCEGS 224
 Db 189 YEEMNKVLLAGKNDKQVGTATLMNQDSSRSHTITIECIEKLESAAAQKPGAKKDSNH 248
 QY 225 VKVSHNLVLDLAGSRAAQTGAAGVRLKEGCNINSLFILQGVIKKLSGQVGGFINYRD 284
 Db 249 VAVGKLVLDLAGSERQDKIGATGRLKEGINKINJSLTALGNVISALVDGK--SGHIPYRD 307
 QY 285 SKLTILQNSLGNPKTRIICTITPV--SFDETLTALQFASAK 326
 Db 308 SKLTILLQDLSGNTKTVWVANIGADWNYDETMTSLRYANRAK 351

RESULT 7

B44259
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
 C:Accession: B44259; S27872
 R:Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
 J. Cell Biol. 119, 1287-1296, 1992
 A:Title: Kinesin family in murine central nervous system.
 A:Reference number: A44259; MUID:93077686; PMID:1447303
 A:Accession: B44259
 A:Molecule type: mRNA
 A:Residues: 1-701 <AIZ>
 A:Cross-references: EMBL:D12645; NID:g220469; PIDN:BAA02166.1; PID:g220470
 A:Experimental source: brain
 A:Note: sequence extracted from NCBI backbone (NCBIP:118911)
 C:Complex: heterodimer with KIF3B (PIR:A57107); the KIF3A/3B heterodimer associates with
 C:Function:
 A:Description: KIF3 complex is a motor protein that provides anterograde fast axonal tra
 C:Superfamily: kinesin-related protein kif3; kinesin motor domain homology
 F:1-368/Domain: head globular #status predicted <HGL>
 F:15-351/Domain: kinesin motor domain homology <KMT>
 F:100-107/Region: nucleotide-binding motif A (P-loop)
 F:349-599/Domain: helical rod #status predicted <ROD>
 F:600-701/Domain: tail globular #status predicted <TGL>
 F:106/Binding site: ATP (Lys) #status predicted

Query Match 38.1%; Score 643; DB 1; Length 701;
 Best Local Similarity 46.2%; Pred. No. 3.1e-41;

Matches 154; Conservative 48; Mismatches 115; Indels 16; Gaps 8;
 QY 6 VAVCVVRPLNREESL--GETAQVYWKTDNNVYQVDSGSGSFGNEDRVFPHGNETTK 59
 DB 15 VKVWVRCRPLNREKSCVQVAVDEMGTITVHKTDSDSNPPKFTFDVTFVGPESKQL 74
 QY 60 NVYEELAAPIDSAIOGYNGTIFAYGQTASGKTYTWGSE---DHLGVIPRAIHDFOKI 116
 DB 75 DVYNLTARPLDSVLENGTIFAYGQTGKTFMEGVRAPVPLGRGVIPNSFAHIFGHI 134
 QY 117 KKPP-DREFLLRVSYMEIYNETITDILCGTQKMKPLIREDVNRVNVYVADLTBEVVYTS 175
 DB 135 AKAGDTRFVRSYLEIYNEERDIL--GDKQTRLEVKERPDVGVITKDLISAYVNNAD 193
 QY 176 MALKWITKGEKSRHYGKTKNORSSRSHITFRMILESREKGEPSNCEGSKVSHLNLVDL 235
 DB 194 DMRIMTLGHKNRSGVATNNHSSRSHALFTITIECEKGVGDGMH--VRMGKHLVDL 251
 QY 236 AGSERAQAGVRLKEGNCINRSLFILGQVTKKLSGQVGFPIFYRDSKLTILONSL 295
 DB 252 AGSERQAKTGATGQRLKEATKINLSLSTLGNVISALVDGK-STHVPYRNSKLTLLQDSL 310
 QY 296 GGNPKTRIITITPV--SPDETTLAQFASTAK 326
 DB 311 GNSKTWMCANIGPADYNYDETITLRYANRAK 343

RESULT 8
 S58691
 A:Residues: 1-742 <RAS>
 A:Note: heterotrimer of a 115K chain and two kinesin-related chains of 85K (PIR:S3898)
 N:Alternate names: kinesin-2 chain B; KRP (85/95) 95K chain
 C:Species: Strongylocentrotus droebachiensis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
 C:Accession: S58691
 R:Rashid, D.J.; Wedaman, K.P.; Scholey, J.M.
 J. Mol. Biol. 252, 157-162, 1995
 A:Title: Heterodimerization of the two motor subunits of the heterotrimeric kinesin, KRP
 A:Reference number: S58691; MUID:95404610; PMID:7674298
 A:Accession: S58691
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA

Query Match 38.1%; Score 642; DB 1; Length 742;
 Best Local Similarity 45.0%; Pred. No. 3.9e-41;
 Matches 150; Conservative 50; Mismatches 117; Indels 16; Gaps 6;
 QY 6 VAVCVVRPLNREESLGETAQVYWKTDNNVYQV-----DGSKSFNEDRVFPHGNETT 58
 DB 9 VKVWVRCRPMNSKEISQGHKRVEMDNKGLVEVTNPKGPPGPKNSFTFDIVYDWSNQ 68
 QY 59 KNVYEELAAPIDSAIOGYNGTIFAYGQTASGKTYTWG---SEDLGVIPRAIHDFOK 115
 DB 69 IDLYDTFRLSVESVLOGNGTIFAYGQTGKTFMEGVRNPELRGVIPNSFEHIFTH 128
 QY 116 IKFPDPREFLLRVSYMEIYNETITDILCGTQKMKPLIREDVNRVNVYVADLTBEVVYTS 175
 DB 129 IARTNQOQLVRSYLEIYQEEIRDLAKDQK-KRLDLKERPDGTGVYVKDLSFVTKSVK 187
 QY 176 MALKWITKGEKSRHYGKTKNORSSRSHITFRMILESREKGEPSNCEGSKVSHLNLVDL 235
 DB 188 EIEHVMVTVGNRVSNGTNNHSSRSHALFTITIESELGVGD--ENHIRVKGKLNLDL 245
 QY 236 AGSERAQAGVRLKEGNCINRSLFILGQVTKKLSGQVGFPIFYRDSKLTILONSL 295
 DB 246 AGSERQAKTGATGQRLKEATKINLSLSTLGNVISALVDGK-SSHIPYRDSKLTLLQDSL 304

QY 296 GGNPKTRIITITPV--FDETTLAQFASTAK 326
 DB 305 GGNAKTVWVANNGPASYNFEDEITITLRYANRAK 337
 RESULT 9
 A54803
 A:Residues: 1-1231 <SEK>
 N:Alternate names: kinesin-related protein KIF4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001
 C:Accession: A54803; D44259
 R:Sekine, Y.; Okada, Y.; Noda, Y.; Kondo, S.; Aizawa, H.; Takemura, R.; Hirokawa, N.
 J. Cell Biol. 127, 187-201, 1994
 A:Title: A novel microtubule-based motor protein (KIF4) for organelle transports, whose
 A:Reference number: A54803; MUID:95014709; PMID:7929562
 A:Accession: A54803
 A:Molecule type: mRNA

A:Residues: 1-1231 <SEK>
 A:Cross-references: GB:D12646; NID:G563772; PIDN:BAA02167.1; PID:dl002657; PID:G563773
 R:Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
 J. Cell Biol. 119, 1287-1296, 1992
 A:Title: Kinesin family in murine central nervous system.
 A:Reference number: A44259; MUID:93077686; PMID:1447303
 A:Accession: D44259
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 91-111, 'S', 113-240 <AIZ>
 A:Experimental source: Brain
 A:Note: sequence extracted from NCBI backbone (NCBIP:118904)
 C:Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
 C:Keywords: ATP; nucleotide binding; P-loop
 F:10-343/Domain: kinesin motor domain homology <KMOT>
 F:88-95/Region: nucleotide-binding motif A (P-loop)

Query Match 38.0%; Score 641.5; DB 2; Length 1231;
 Best Local Similarity 44.3%; Pred. No. 8.4e-41;
 Matches 147; Conservative 53; Mismatches 115; Indels 17; Gaps 7;
 QY 6 VAVCVVRPLNREESLG-ETAQVYWKTDNNVYQVDSGSKSFNEDRVFPHGNETTKNVYEE 64
 DB 10 VRVALRCRPLVSKHEIKGQCQLCSFVGPQV--VGNDKSFTYDFVDPSTEQEVNT 67
 QY 65 IAAPIIDSAIOGYNGTIFAYGQTASGKTYTWGSGS---EDH---LGVIPRAIHDFOKIK 117
 DB 68 AVAPLKGFGYNATVLAGYGTGSGKTYSMGGAYTAQEHDSALGIVPRVQLLFKEIN 127
 QY 118 KPDPREFLLRVSYMEIYNETITDILCGT-QKMKPLIREDVNRVNVYVADLTBEVVYTS 176
 DB 128 KKSDFEFLRVSYLEIYNEEILDLCSREKATQINREDPKKGKIVGLIEKTVLVASD 187
 QY 177 ALKWTIKGEKSRHYGKTKNORSSRSHITFRMILESREKGEPSNCEGSKVSHLNLVDLA 236
 DB 188 TVSCLEQGNERTVASTAMNSQSSRSHALFTISIEQRKK---NDKNSFRSKLHLVDLA 243
 QY 237 GSERAAQAGVRLKEGNCINRSLFILGQVTKKLSGQVGFPIFYRDSKLTILONSLG 296
 DB 244 GSERQKTKAEGDRLREGININRGLLCLGNVISALGDDKKGNFVYRDSKLTLLQDSL 303
 QY 297 GNPKTRIITITPV--SPDETTLAQFASTAK 326
 DB 304 GNSHTIMTACVSPADSNLEETLTLRYADRAR 335
 RESULT 10
 H86350
 A:Residues: 1-1742 <RAS>
 N:Alternate names: kinesin-related protein F9K7.17 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C:Accession: H86350
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.
 ansen, N.F.; Hughes, B.; Huizar, L.

Query Match	37.4%	Score 630;	DB 1;	Length 747;
Best Local Similarity	43.8%	Pred. No. 3.3e-40;		
Matches 147;	Conservative 54;	Mismatches 115;	Indels 20;	Gaps 7;

QY	5	AVAVCVVRPLNSREESLG-----ETAAQVTKTKDNNVIYQVDSKSFNFQVRPHGN	55
DB	9	SVRVVRCRPNWGEKKAASVDKVDVKLGQGVSKVKNPKGTSHEM--PKTFTFDVAVDWN	66
QY	56	ETTKNVYEEIAAPLIDSAIQCYNGTIFAYGQTASGKTYTM--MGSDHLGVIPRAIHDI	112
DB	67	AKQPELYDETFRPLAVDSVLQFNGTIFAYGQTGKTYTMGEVGRDPEKRGVIPNSFDHI	126
QY	113	FQIKKPPDREFLLRVSMYIYNETIDLLCGTQWKPLIIRVDVNRNVYVADLTBEVVY	172
DB	127	FTHISRSONQYIVRASLYEIOBEIRDLLSKQD--TKRLKLRPDTGVVVKDLSSPVTK	195
QY	173	TSEMALKWITKGBKSRHYGTCKNORSSRSHITFRMLLESREKGFSPNCGSVKVSHLNL	232
DB	186	SVKEIEHVMVGNQSVRGATNNWESSRSHALFVITIECSVG--LDGENHIVRGKLN	243
QY	233	VDLAGSERAQTAGAAGVRLKEGNCINRSLFILQGVTKLSDGQGVGFNVDRDCKLRLIQ	292
DB	244	VDLAGSERAQTAGAAGVRLKEGNCINRSLFILQGVTKLSDGQGVGFNVDRDCKLRLIQ	302
QY	293	NSLGGNPKTRIICTITPVGF--DETLTALQFASAK	326
DB	303	DSLGGNAKTVMANVGNPASTVNEETLTILRYANRAK	338

RESULT 12

IS1617

kinesin-like protein 1 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 02-Feb-2001

C:Accession: IS1617; A48835; S48837

C:Vernos, I.; Raats, J.; Hirano, T.; Heasman, J.; Karsenti, E.; Wylie, C. Cell 81, 117-127, 1995

A:Title: Xklp1, a chromosomal Xenopus kinesin-like protein essential for spindle

A:Reference number: A56221; MUID:95236444; PMID:7720067

A:Accession: IS1617

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1226 <VER>

A:Cross-references: EMBL:X82012; NID:G562792; PIDN:CAA57539.1; PID:G562793

R:Vernos, I.; Heasman, J.; Wylie, C. Dev. Biol. 157, 232-239, 1993

A:Title: Multiple kinesin-like transcripts in Xenopus oocytes.

A:Reference number: A48835; MUID:93246065; PMID:8482413

A:Accession: A48835

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 9-162,'L',164-338 <VE2>

A:Experimental source: oocyte

A>Note: sequence extracted from NCBI backbone (NCBIP:130975)

C:Genetics:

A:Gene: klp1

C:Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology

C:Keywords: ATP; nucleotide binding; p-loop

C:Keywords: F.9-343/Domain: kinesin motor domain homology <XMOF>

A:Region: 87-94/Region: nucleotide-binding motif A (p-loop)

Query Match	37.3%	Score 628.5;	DB 2;	Length 1226;
Best Local Similarity	44.1%	Pred. No. 8.3e-40;		
Matches 149;	Conservative 53;	Mismatches 117;	Indels 19;	Gaps 9;

QY	2	EAG-AVAVCVVRPLNSRESLG-ETAAQVTKTKDNNVIYQVDSKSFNFDRVPHGN	59
DB	4	DEGIPVRVALRCRPLVPKENNECKMCLTFVPPGQQVI--VGTEKSTYDVFDP	61
QY	60	NVYEEIAAPLIDSAIQCYNGTIFAYGQTASGKTYTMWGSDEH-----LGVIPRAIHDI	112
DB	62	EVNSAVAPLKLFGYNATVLAICYGTGSKTYSNGAYTHNQNEPTVGIPRTVIAL	121

113 FOKIKKPPDEFLLRVSYMEIYNETITDIL-CGTQMKKFLIREDVNRNVYADLTVEV 171
 122 FREIHPQWENFLKVSLEYINEELDLAARDKNTIREDPKGKICGLTERDV 181
 172 YTSALKWITTKGKSRHYGETKMNORSRSHITFPMILESRKGPSPCEGSKVSHLN 231
 182 KTAIDTLSCLEQNSRSTVASTAMNSQSSRSHAITFISIEQRKEGDKNN---SFR-SKLH 237
 232 LVDLAGSRAAQTGAAGVRLKEGCNINRSIFILGOVKKLSD-GQVGGFINYRDSKLTRI 290
 238 LVDLAGSERQKTKAEDRUKGIGISNRGLLGNVISALGDSKKGFPYRDSKLTRL 297
 291 LQNSLGNPKTRIICTITPV--SFDETLTALQFASAK 326
 298 LQDSLGNSHYLMACVSPADSNMEETLNTLRVADRAR 335

RESULT 13
 S38982
 kinesin-related protein KRP85 - sea urchin (Strongylocentrotus purpuratus)
 N:Alternate names: kinesin-2 chain A; KRP (85/95) 85K chain
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
 C:Accession: S38982; S72551
 R:Cole, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.; Scholey, J.M.
 Nature 366, 268-270, 1993
 A:Title: Novel heterotrimeric kinesin-related protein purified from sea urchin eggs.
 A:Reference number: S38982; MUID:94050179; PMID:8232586
 A:Accession: S38982
 A:Molecule type: mRNA
 A:Residues: 1-699 <COL1>
 A:Cross-references: EMBL:L16993; NID:g295245; PIDN:AAA16098.1; PID:g295246
 A:Accession: S72551
 A:Molecule type: protein
 A:Residues: 2-5, 'X', 7-11, 59-64, 125-132, 222-226, 'X', 228-230 <COL2>
 C:Complex: heterotrimer of a 115K chain and two kinesin-related chains of 55K (PIR:S5869)
 C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
 C:Keywords: ATP; heterotrimer; microtubule binding; nucleotide binding; P-loop
 F:1-348/Domain: kinesin motor domain homology <KWOT>
 F:97-104/Region: nucleotide-binding motif A (P-loop)
 F:103/Binding site: ATP (lys) #status predicted

Query Match 37.0%; Score 623.5; DB 1; Length 699;
 Best Local Similarity 46.2%; Pred. No. 9.4e-40;
 Matches 156; Conservative 47; Mismatches 110; Indels 25; Gaps 10;

QY 6 VAVCVVRPLNSRRESLG-----ETAQVYWKTDNNVIYQVDGSKSFNDRVPHG 54
 DB 11 VRVVRCPRLNSKETGQGFKSVVKMDMRGTQV---TNPNA-PSGEPPKSTFDIVFAP 66
 QY 55 NETTKNVYEIAPIIDSAIQVNGTIFAYGQTASGKTYTMMG--SEDLH-GVIPRAIHD 111
 DB 67 GAKQTDVYVQTRPIVDALIEGNGTIFAYGQTGKTFTMEGVRSQPELRGIIPNSFAH 126
 QY 112 IFQIKKKFPDR-EFLLRVSYMEIYNETITDLCGTQMKKFLIREDVNRNVYADLTVEV 170
 DB 127 IFGHIAKEQENRFLRVSYLEYINEEVKDLL-GKQQRHLEVKRDPVGVYKDLISAFV 185
 QY 171 VYTSEMAKWIYTKGKSRHYGETKMNORSRSHITFPMILESRKGPSPCEGSKVSHL 230
 DB 186 VNNADMDRIMTLGNKNRSVGTATNMNESSRSRTAIFITLERSDMG--LDKEQHVAVGKL 243
 QY 231 NLVDLAGSRAAQTGAAGVRLKEGCNINRSIFILGOVKKLSDGQVGGFINYRDSKLTRI 290
 DB 244 HMDLAGSERQTKGTGQELKEATKINLSLTGLNVISSILVDGK-STHPIYRNSKLTRL 302
 QY 291 LQNSLGNPKTRIICTITPV--SFDETLTALQFASAK 326
 DB 303 LQDSLGNNAKTVMCANIGPAEYNYDETISTLRVANRAK 340

RESULT 14
 T49235

kinesin-like protein - Arabidopsis thaliana
 N:Alternate names: protein F7K15.60
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T49235
 R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25019
 A:Accession: T49235
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-932 <OBE>
 A:Cross-references: EMBL:AL353871; GSPDB:GNO0061; ATSP:F7K15.60
 A:Experimental source: cultivar Columbia; BAC clone F7K15
 C:Genetics:
 A:Gene: ATSP:F7K15.60
 A:Map position: 3
 A:Introns: 76/1; 106/1; 139/3; 177/3; 205/1; 227/3; 247/3; 289/2; 355/3; 401/3; 430/3;

Query Match 36.8%; Score 621; DB 2; Length 932;
 Best Local Similarity 44.6%; Pred. No. 2.1e-39;
 Matches 148; Conservative 54; Mismatches 110; Indels 20; Gaps 8;

QY 3 EGAVAVCVVRPLNSRRESLGETAQVYWK--TDNNVIYQ----VDGSKSFNDRVPHGNE 56
 DB 26 EEKILVTVMRPLNWRHAKYDL--IAWECDDDTIVFKPNPDKAPTKYDFKVFETC 83
 QY 57 TTKNVYEIAPIIDSAIQVNGTIFAYGQTASGKTYTMMGSEDLHGVIPRAIHDFOKI 116
 DB 84 ATQEVYEGGRDVALSALAGTNATIFAYGQTSCKTFTMR-----GVTESWVKDIYBHI 137
 QY 117 KKFDPDRFLLRVSYMEIYNETITDLCGTQMKKFLIREDVNRNVYADLTVEVYVVTSEM 176
 DB 138 RKTQERSFLVKVSALEYINVTWDL--NRDTGLRLDLDPEKGTIVENLVEEVVESQKH 195
 QY 177 ALKWITKGEKSRHYGETKMNORSRSHITFPMILESRKGPSPCEGSKVSHLMLVDLA 236
 DB 196 LQHLISICEDQVQVGETALNDKSRSHOILRLTHSSLR-ELAGCVQSF-MATLNLVDLA 253
 QY 237 GSERAAQTGAAGVRLKEGCNINRSIFILGOVKKLSDGQVGGFINYRDSKLTRILQNSLG 296
 DB 254 GSERAFQTNADGLRLKEGSHINRSLLTTLTVIRKSSGKRDRHVPYRDSKLTRILQNSLG 313

QY 297 GNPKTRIICTITPV--SFDETLTALQFASAK 326
 DB 314 GNARTALICTISPALSHVEQTKKTLSPFMSAK 345

RESULT 15
 T06065
 hypothetical protein F19H22.150 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 31-Mar-2000
 C:Accession: T06065
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15184
 A:Accession: T06065
 A:Molecule type: DNA
 A:Residues: 1-1121 <BEV>
 A:Cross-references: EMBL:AL035679; GSPDB:GNO0062; ATSP:F19H22.150
 A:Experimental source: cultivar Columbia; BAC clone F19H22
 C:Genetics:
 A:Gene: ATSP:F19H22.150
 A:Map position: 4
 A:Introns: 139/2; 170/1; 200/1; 256/3; 284/3; 302/3; 322/3; 349/1; 371/3; 390/3; 425/3;
 C:Superfamily: kinesin heavy chain; kinesin motor domain homology
 F:99-494/Domain: kinesin motor domain homology <KWOT>

Query Match 36.7%; Score 618.5; DB 2; Length 1121;
 Best Local Similarity 39.4%; Pred. No. 4.3e-39;
 Matches 158; Conservative 58; Mismatches 102; Indels 83; Gaps 12;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 09:26:36 ; Search time 3.15048 Seconds
(without alignments)

5421.082 Million cell updates/sec

Title: US-10-045-631B-88_COPY_2_329

Perfect score: 1686

Sequence: 1 AEEGAVAVCVRVPLNSREE.....PVSFDETLALQFATAKYM 328

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1686	100.0	2663	1	CENE HUMAN
2	650	38.6	786	1	FL10_CHLRE
3	644	38.2	702	1	KF3A_HUMAN
4	643	38.1	701	1	KF3A_MOUSE
5	643	38.1	1232	1	KF4A_HUMAN
6	642	38.1	742	1	KI21_STRPU
7	641.5	38.0	1231	1	KF4A_MOUSE
8	631	37.4	747	1	KF3B_HUMAN
9	630	37.4	747	1	KF3B_MOUSE
10	628.5	37.3	1226	1	KF4A_XENLA
11	624.5	37.0	1029	1	KI17_HUMAN
12	623.5	37.0	699	1	KI22_STRPU
13	613.5	36.4	1038	1	KI17_MOUSE
14	608	36.1	1225	1	KF4A_CHICK
15	605	35.9	672	1	OSN3_CAEEL
16	593.5	35.2	975	1	KINH_DROME
17	591.5	35.1	1031	1	KINH_STRPU
18	591.5	35.1	1584	1	U104_CAEEL
19	588	34.9	1749	1	KI3A_MOUSE
20	586.5	34.8	554	1	KLP3_SCHPO
21	585	34.7	793	1	KF3C_HUMAN
22	584	34.6	796	1	KF3C_RAT
23	584	34.6	1805	1	KI3A_HUMAN
24	583	34.6	963	1	KINH_MOUSE
25	582	34.5	796	1	KF3C_MOUSE
26	582	34.5	928	1	KINH_NEUCR
27	582	34.5	963	1	KINH_HUMAN
28	582	34.5	1066	1	KI61_DROME
29	580.5	34.4	1032	1	KINN_HUMAN
30	578.5	34.3	1027	1	KINN_MOUSE
31	578.5	34.3	1826	1	KI3B_HUMAN
32	578	34.3	957	1	KF5C_HUMAN
33	576.5	34.2	967	1	KINH_LOUPE

34 575.5 34.1 378 1 KLP2_BOMMO
35 574 34.0 956 1 KF5C_MOUSE
36 571.5 33.9 935 1 KINH_SYNRA
37 570 33.8 1690 1 KF1A_HUMAN
38 569 33.7 815 1 KINH_CAEEL
39 568 33.7 784 1 KLP6_DROME
40 568 33.7 1695 1 KF1A_MOUSE
41 561 33.3 1648 1 KF14_HUMAN
42 557 33.0 1816 1 KF1B_MOUSE
43 547 32.4 1103 1 KF1C_HUMAN
44 539.5 32.0 1056 1 KI25_ARATH
45 538 31.9 1067 1 BG52_XENLA

P46874 bombyx mori
P28738 mus musculus
Q43093 synccephalas
Q12756 homo sapien
P34540 caenorhabdi
P46867 drosophila
P33173 mus musculus
Q15058 homo sapien
Q60575 mus musculus
O43896 homo sapien
P82266 arabidopsis
Q91783 xenopus lae

ALIGNMENTS

RESULT 1
CENE HUMAN
ID CENE HUMAN STANDARD; PRT; 2663 AA.
AC Q02224;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Centromeric protein E (CENP-E protein).
GN CENPE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024922; PubMed=1406971;
RA Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
RT "CENP-E is a putative kinetochore motor that accumulates just before
RT mitosis.";
RL Nature 359:536-539(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95196755; PubMed=7889940;
RA Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RL microtubule motor.";
RN EMBO J. 14:918-926(1995).
RP CHARACTERIZATION.
RX MEDLINE=98437347; PubMed=9763420;
RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
RL interactions with the kinetochore proteins CENP-F and hBUBR1.";
RN J. Cell Biol. 143:49-63(1998).
RP FARNESYLATION.
RX MEDLINE=20459117; PubMed=10852915;
RA Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong L.,
RT Bishop W.R., Kirschmeier P.;
RT "Farnesyl transferase inhibitors block the farnesylation of CENP-E
RL and CENP-F and alter the association of CENP-E with the
RN microtubules.";
RX J. Biol. Chem. 275:30451-30457(2000).
RP FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC KINETOCORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
CC AND/OR SPINDLE ELONGATION.
RP SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
RP SIMILARITY: Belongs to the kinesin-like protein family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; Z15005; CAA78727.1; -.
 PIR; S28261; S28261.
 R R HSSP; F17119; 3KAR.
 R R Genew; HGNC:1856; CENPE.
 R R GK; Q0224; -.
 R R MIM; 117143; -.
 R R GO; GO:0005699; C:kinetochore; TAS.
 R R GO; GO:0005634; C:nucleus; TAS.
 R R GO; GO:0008350; F:kinetochore motor activity; TAS.
 R R GO; GO:0000067; F:DNA replication and chromosome cycle; TAS.
 R R GO; GO:0007079; P:mitotic chromosome movement; TAS.
 R R GO; GO:0007080; P:mitotic metaphase plate congression; TAS.
 R R InterPro; IPR001752; kinesin_motor.
 R R Pfam; PF00235; kinesin; 1.
 R R PRINTS; PR00380; KINESINHEAVY.
 R R SMART; SM00129; KISC; 1.
 R R PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 R R PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
 R R W W Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
 W W Cell cycle; Centromere; Lipoprotein; Prenylation.
 W W DOMAIN 1 335 KINESIN-MOTOR.
 W W DOMAIN 335 2471 COILED COIL (POTENTIAL).
 W W DOMAIN 2472 2663 GLOBULAR (POTENTIAL).
 T T NP BIND 86 93 ATP (BY SIMILARITY).
 T T LIPID 2660 2660 S-farnesyl cysteine.
 T T SEQUENCE 2663 AA; 312087 MW; CECF13880C8CB8 CRC64;
 T T

Query Match	100.0%;	Score 1686;	DB 1;	Length 2663;
Best Local Similarity	100.0%;	Pred. No. 2.5e-121;		
Mismatches	0.	Mismatches	0.	Indels 0;
Gaps	0;			

	QY	1	AEEGAVACVVRVPLNSRRESLGETHAQVTWKTDNNVIYQVDGSKSFNDRVPFHGNETTKN	60
	DB	2	AEEGAVACVVRVPLNSRRESLGETHAQVTWKTDNNVIYQVDGSKSFNDRVPFHGNETTKN	61
	QY	61	VYEELAAPIIDSALIQYNGTIPAYGQTASGKTYTWMGSEDLHGVIPRAIHDIFQIKKFP	120
	DB	62	VYEELAAPIIDSALIQYNGTIPAYGQTASGKTYTWMGSEDLHGVIPRAIHDIFQIKKFP	121
	QY	121	DREFLRVSVMEIYNETITDLCGTQMKPLIIREDVNRNVYADLTBEVVYTSMAWKW	180
	DB	122	DREFLRVSVMEIYNETITDLCGTQMKPLIIREDVNRNVYADLTBEVVYTSMAWKW	181
	QY	181	ITKGEKRHYGETKMQRSSRSHTIPFMILSREKGEPCNCEGSVKVSHNLVLDLAGSR	240
	DB	182	ITKGEKRHYGETKMQRSSRSHTIPFMILSREKGEPCNCEGSVKVSHNLVLDLAGSR	241
	QY	241	AAQTGAAGVPLKEGCNINRSLFILGOVITKKLSOGVGGFINYRDYSKLTRILQNSLGCNPX	300
	DB	242	AAQTGAAGVPLKEGCNINRSLFILGOVITKKLSOGVGGFINYRDYSKLTRILQNSLGCNPX	301
	QY	301	TRIICTTTPVSFDFTLAFASTAKYM	328
	DB	302	TRIICTTTPVSFDFTLAFASTAKYM	329

RESULT 2			
REFL10	CHLRE	STANDARD;	PRT; 786 AA.
FL10	CHLRE		
P46869;			
AC			
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	01-OCT-1996 (Rel. 34, Last annotation update)		
DE	Kinesin-like protein FLA10 (KHP1 protein).		
GN	FLA10.		
OS	Chlamydomonas reinhardtii.		
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;		
OC	Chlamydomonadaceae; Chlamydomonas		

```

NCBI_TaxID=3055;
[1]
RN      SEQUENCE FROM N.A.
RP
RC      STRAIN=137;
RC      MEDLINE=94299638; PubMed=8027176;
RC      MEDLINE=94299638; PubMed=8027176;
RT      Walther Z., Vashishtha M., Hall J.L.;
RT      "The Chlamydomonas FlA10 gene encodes a novel kinesin-homologous
RT      protein.";
RT      J. Cell Biol. 126:175-188(1994).
CC      !- FUNCTION: Probably involved in flagellar assembly and maintenance.
CC      !- TISSUE SPECIFICITY: Flagellar axoneme.
CC      !- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC      II SUBFAMILY.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).

```

CC	EMBL:	L33697;	AAA21738.1;	-.
DR	PIR:	A53939;	A53939.	
DR	HSSP:	P17119;	3KAR.	
DR	InterPro:	IPR001752;	kinesin_motor.	
DR	Pfam:	PF00225;	kinesin; 1.	
DR	PRINTS:	PR00380;	KINESINHEAVY.	
DR	SMART:	SM00129;	KISC; 1.	
DR	PROSITE:	PS00411;	KINESIN MOTOR DOMAIN1; 1.	
DR	PROSITE:	PS50067;	KINESIN MOTOR DOMAIN2; 1.	
KW	Motor protein;	Microtubule;	ATP-binding; ATP-binding; KINESIN-MOTOR (BY SIMILARITY).	
FT	DOMAIN	1	358	KINESIN-MOTOR (BY SIMILARITY).
FT	DOMAIN	367	687	COILED COIL (POTENTIAL).
FT	DOMAIN	688	786	GLOBULAR (POTENTIAL).
FT	NP BIND	97	104	ATP (POTENTIAL).
FT	DOMAIN	388	391	POLY-GLY.
FT	DOMAIN	705	714	POLY-GLY.
FT	DOMAIN	756	759	POLY-ASP.
SO	SEQUENCE	786	AA: 86671 MW: F90969203EB79FF1B	CRC64;

Query Match	38.6%;	Score 650;	DB 1;	Length 786;	
Best Local Similarity	44.9%;	Pred. No. 2.6e-42;			
Matches	154;	Conservative 56;	Mismatches 110;	Indels 24;	Gaps 8;
Qy	5	AVAVCVRVPLNSRESFSLGETAQVYWKTDNNVY----	QVDGS----	KSFNFDPRVFHNET	57
Db	10	SVKVVVRCRPLNGKEKADGSRIVDMVDVDAQVKVRNPKADASEPPKAFITDQVYDNNQC			69
Qy	58	TKNVEYIEAAPIDSAIQGNGTIFAYGQTASGKTYTMGSEDH----	LGVIPIRAIHIFQ		114
Db	70	QRDVFDTIAPRLIDSCIEGYNGTIFAYGQTGKSHTEGKDEPPELRGLIPNTRFYVFE			129
Qy	115	KI-KKFPDRFLLRVSVWEIYNETITDLCGTQWKPLIREDVNRVYVADLVEEVVYT			173
Db	130	IIARDSGTKEFLVRSYLEYINEVRDLL-GKHSKKMELKESPRGVYVYKLSQFVCKN			188
Qy	174	SEMAKWLITKEKSRHGYETKONQSRSHIIPRMILESREK-----	GEPSNCEGS		224
Db	189	YEEMNKVLLAGKNRVGATILNQDSRSHSIFITITIEKLESAAAKPGAKKDDSNH			248
Qy	225	VKVSHLNLVDLAGSERAQOTGAAGVRUKEGGNINRSFILGQVTKKLSDGQVGGFINYRD			284
Db	249	VRVGKLNLDLAGSERQDKTATGDRUKEGH KINLSLTALGNVISALVDGK-SGHIPYRD			307
Qy	295	SKLTPRILONSIGGNPKTRILCTITPV--SPDETITLALQFASAK			326
Db	308	SKLTLLQDSLGGNKTVMQVANIGAPADWNVDWTSLRYANRAK			351

RESULT 3

KE3A HUMAN

ID KF3A_HUMAN STANDARD; PRT; 702 AA.
 AC Q9Y496; Q86XE9; Q9Y6V4;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kinesin-like protein KIF3A (Microtubule plus end-directed kinesin motor 3A).
 GN KIF3A OR KIF3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=20018159; PubMed=10548469;
 RA Whitehead J.L., Wang S.Y., Bost-Usinger L., Hoang E., Frazer K.A., Burnside B.;
 RA "Photoreceptor localization of the KIF3A and KIF3B subunits of the heterotrimeric microtubule motor kinesin II in vertebrate retina."; Exp. Eye Res. 69:491-503(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A., Huetting J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP SEQUENCE FROM N.A.
 RA Connolly K.S., Gunning K.M., Davis C.A., Kadner K., Subramanian S., Miguel T., Lewis K.D., Fridlyand J., Alcivare D., Benke J.A., Bondoc M., Bowen E., Chiang A., Critz P., Jaklevic M.A., Lindo K., Lindquist K., Miller C., Patel S., Piscia C., Riley B.E., Rojeski H., Sarmiento R., Yu C., Montenegro M., Aerts A., Chung A., Abrajano A., Baker M., Gao C., Jett J., Ko C., Beall K., Woolley J.P., Stultz J.L., Kimmery W., Martin C.H.;
 RA "Sequencing of human chromosome 5".
 RN Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLATOR FOR MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE GUIDING ACTIVITY IN VITRO.
 CC -1- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous gene model prediction.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC

J. Cell Biol. 119:1287-1296(1992).
 CC FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLATOR FOR
 CC MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING
 CC ACTIVITY IN VITRO.
 CC SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
 CC TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN ADULT BRAIN
 CC TISSUE (MAINLY IN THE CEREBELLAR GRANULAR LAYER) WITHIN A SINGLE
 CC TYPE OF NEURONAL CELL.
 CC SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC II SUBFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: D12645; BAA02166.1; -.
 CC PIR: B44259; B44259.
 CC HSP: P17119; 3KAR.
 CC MGD: MGI:107689; Kif3a.
 CC InterPro: IPR001752; kinesin_motor.
 CC Pfam: PF00225; kinesin; 1.
 CC PRINTS: PR00380; kinesin.
 CC SMART: SM00129; KISC; 1.
 CC PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
 CC PROSITE: PS00067; KINESIN MOTOR DOMAIN2; 1.
 CC Motor protein; Microtubule; ATP-binding; Coiled coil; Neurone.
 CC FT DOMAIN 1 350 KINESIN-MOTOR (BY SIMILARITY).
 CC FT DOMAIN 351 598 COILED COIL (BY SIMILARITY).
 CC FT NP BIND 100 107 ATP (BY SIMILARITY).
 CC FT DOMAIN 442 445 POLY-GLU.
 CC FT DOMAIN 509 512 POLY-ARG.
 CC FT SEQUENCE 701 AA; 801.67 MW; 2405872DFD2D95A29 CRC64;
 CC
 CC Query Match 38.1%; Score 643; DB 1; Length 701;
 CC Best Local Similarity 46.2%; Pred. No. 7.6e-42;
 CC Matches 154; Conservative 48; Mismatches 115; Indels 16; Gaps 8;
 CC
 CC QY 6 VAVCVVRPLNSRESL--GETAQYWKTDNNVYQVDGS---KSNFDRVEHGNETK 59
 CC DB 15 KVAVVRCPLNREKSMYQVAVDEMRGTTVHKTDSSNEPKTFTFDVFGPEKQL 74
 CC QY 60 NYVEELAPITDSATGYNGTIFAYGQTASGKTYTMGSE---DHLGVIPRAIHDFOKI 116
 CC DB 75 DVYNLTARPIIDSVLENGTIFAYGQTGKTFTMEGVRAVPLGLGVIPNSFAHIFGHI 134
 CC QY 117 KKFP--DREFLLRVSYMEIYNETITDLCGTQMKPLIITREDVNRNYYVADLTFEYVYTS 175
 CC DB 135 AKAEQDTRFLRVSYLYEINVEVRDL--GKQDQRLVLRKPDVGVYIKDL SAYVYNNAD 193
 CC QY 176 MALKWITGEKRRHGETKQNRSSRSRTIFRMILESEKGEPSCEGSKVSHLNVL 235
 CC DB 194 DMDRINTLGHKNRSVGATNMNEHSHSRAIFTITCEKGVGDGNH--VRMGKHLHVL 251
 CC QY 236 AGSRAAOTGAAGVRLKECCNINRSILFGLGVKILSDGVGVGFNYRDSKLTRELQNSL 295
 CC DB 252 AGSEQAQKATGQRLKEATKINLSLSTLGNVISALVDGK--STHVPYRNSKLTRELQNSL 310
 CC QY 296 GGNPKTRICTITPV--SPDETALQFASTAK 326
 CC DB 311 GGNSTKMTMCANIGPADYNYDETISTILRYANRAK 343
 CC
 CC RESULT 5
 CC KF4A HUMAN STANDARD; PRT; 1232 AA.
 CC AC Q95239; Q9NNY6; Q9NNY24; Q9NMW3;
 CC DT 15-JUL-1999 (Rel. 38, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chromosome-associated kinesin KIF4A (Chromokinesin).
 GN KIF4A OR KIF4
 OS Homo sapiens (Human).
 ON Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RA Villard L.;
 RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RP MEDLINE=20435301; PubMed=10978527;
 RX On S.J., Hahn H., Torrey T.A., Shin H., Choi W., Lee Y.M.,
 RA Morse H.C. III, Kim W.;
 RA "Identification of the human homologue of mouse KIF4, a kinesin
 RT superfamily motor protein.";
 RT Biochim. Biophys. Acta 1493:219-224 (2000).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Retinoblastoma;
 RC Rentsch A., Neumann T., Rommerskirch W.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN SEQUENCE OF 128-1232 FROM N.A.
 RP TISSUE=Retinoblastoma;
 RC MEDLINE=97311419; PubMed=9168136;
 RX Yan R.-T., Wang S.-Z.;
 RA "Increased chromokinesin immunoreactivity in retinoblastoma cells.";
 RL Gene 189:263-267 (1997).
 CC -!- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOLAR
 CC SPINDLE STABILIZATION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear. Associated with mitotic
 CC chromosomes (By similarity).
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEMATOPOIETIC TISSUES,
 CC FETAL LIVER, SPLEEN, THYMUS AND ADULT THYMUS AND BONE MARROW.
 CC LOWER LEVELS ARE FOUND IN HEART, TESTIS, KIDNEY, COLON AND LUNG.
 CC -!- SIMILARITY: Belongs to the kinesin-like protein family.
 CC Chromokinesin subfamily.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF179308; AAD51855.1; -.
 CC DR EMBL: AF071592; AAD05492.2; -.
 CC DR EMBL: AJ271784; CAB75427.1; -.
 CC DR EMBL: AF277375; AAF86334.1; -.
 CC HSP: P17119; 3KAR.
 CC Genew; HGNC:13339; KIF4A.
 CC GO: GO:0005737; C:cytoplasm; TAS.
 CC GO: GO:0005876; C:spindle microtubule; TAS.
 CC GO: GO:0003777; F:microtubule motor activity; TAS.
 CC GO: GO:0008089; P:anterograde axon cargo transport; TAS.
 CC GO: GO:0006996; P:organelle organization and biogenesis; TAS.
 CC InterPro: IPR001752; kinesin_motor.
 CC Pfam: PF00225; kinesin; 1.
 CC PRINTS: PR00380; kinesin.
 CC SMART: SM00129; KISC; 1.
 CC PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
 CC PROSITE: PS00067; KINESIN MOTOR DOMAIN2; 1.
 CC Motor protein; Microtubule; ATP-binding; DNA-binding;
 CC Nuclear protein; Coiled coil.
 CC FT DOMAIN 1 349 KINESIN-MOTOR.
 CC FT DOMAIN 350 999 COILED COIL (BY SIMILARITY).
 CC FT DOMAIN 1000 1232 GLOBULAR.
 CC FT NP_BIND 88 95 ATP (POTENTIAL).
 FT

FT CONFLICT 223 233 R -> G (IN REF. 2).
 FT CONFLICT 231 231 S -> T (IN REF. 4).
 FT CONFLICT 286 286 V -> A (IN REF. 2).
 FT CONFLICT 422 422 L -> W (IN REF. 2).
 FT CONFLICT 564 564 L -> H (IN REF. 4).
 FT CONFLICT 564 564 L -> P (IN REF. 2).
 FT CONFLICT 600 600 K -> E (IN REF. 3).
 FT CONFLICT 658 658 R -> K (IN REF. 3 AND 4).
 FT CONFLICT 928 928 Q -> P (IN REF. 1).
 FT CONFLICT 958 958 Q -> R (IN REF. 3).
 FT CONFLICT 960 960 L -> Q (IN REF. 1).
 FT CONFLICT 996 997 LL -> S (IN REF. 4).
 FT CONFLICT 1003 1014 QKHLPKDTLLSP -> RLPRIIPFYLQ (IN REF. 4).
 FT CONFLICT 1022 1022 P -> Q (IN REF. 2).
 FT CONFLICT 1077 1077 K -> N (IN REF. 2).
 FT CONFLICT 1138 1138 G -> S (IN REF. 2).
 SQ SEQUENCE 1232 AA; 139908 MW; FF74052A17A8B8F7 CRC64;
 Query Match 38.1%; Score 643; DB 1; Length 1232;
 Best Local Similarity 44.4%; Pred. No. 1.6e-41;
 Matches 147; Conservative 51; Mismatches 117; Indels 16; Gaps 5;
 QY 6 VAVCVVRVPLNSREESLG-ETAQVYKTDNNVIQVVDGSKSENFDRVFHGHGNETTKVYEE 64
 Db 10 VRVALRCRPLVPKEISGQWCLSFVPGEPQVVGTD--KSFTYDFVDFPSTQEVFNT 67
 QY 65 IAAPIIDSAIQNGNFIAYGTQASGKTYTMMG-----SEDLGVIPRAIHDIKOK 117
 Db 68 AVAPLKGKFGKYNATVLAAYGTGSGKTYSMGAYTAQENETVGVIPRVIQLLKEID 127
 QY 118 KFPDFEFLRVSYMEIYNETITLLCGTQMKPLIREDVNRVYVADLTREVVYTSMA 177
 Db 128 KKSDFEFLRVSYMEIYNETITLLCGTQMKPLIREDVNRVYVADLTREVVYTSMA 177
 QY 178 LKWTIKGKSRHYGETKMQRSRSHITFRMILESEKGEPSNCEGSKVSHLNLVDLAG 237
 Db 188 VSCLEGGNSRIVASTAMNSQSSRSHAITISLEQRKSD----KNSFSRKLHLVDLAG 243
 QY 238 SERAQTGAAGVRLKEGCNINSLFILGQVVKLSGQVGGFINVRDYSKLTILQNSLGG 297
 Db 244 SERQKTKAEGRLKEGININRGLLCLGNVISALGDDKGGFVPRYDSKLTILQNSLGG 303
 QY 298 NPKTRIICITPV--SFDLTLALQFASAK 326
 Db 304 NSHTLMIACVSPADNLEETLTLAYADR 334

RESULT 6
 KI21_STRPU
 ID KI21_STRPU STANDARD; PRT; 742 AA.
 AC P46871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kinesin-II 95 kDa subunit (KRP-85/95 95 kDa subunit).
 GN KRP95.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Egg;
 EX MEDLINE=94050179; PubMed=8232586;
 RA Cole D.G., Chinn S.W., Wedaman K.P., Hall K., Vuong T.,
 RA Scholey J.M.;
 RT "Novel heterotrimeric kinesin-related protein purified from sea
 RT urchin eggs";
 RL Nature 366:268-270(1993).
 CC -1- SUBUNIT: Heterotrimer of a 115 kDa subunit (KAP115) and two
 CC kinesin-like subunits of 95 kDa (KRP95) and 85 kDa (KRP85).
 CC -1- PTM: The N-terminus is blocked.

CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC II SUBFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U00996; AAA87393.1; -;
 DR HSSP; P17119; 3KAR.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; kinesin; 1.
 DR PRINTS; PRO0380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN; 1.
 DR PROSITE; PS00667; KINESIN MOTOR DOMAIN; 1.
 KW Motor protein; Microtubule; ATP-binding; Coiled coil.
 FT DOMAIN 1 337 KINESIN-MOTOR (BY SIMILARITY).
 FT DOMAIN 338 613 COILED COIL (BY SIMILARITY).
 FT DOMAIN 614 742 GLOBULAR (BY SIMILARITY).
 FT NP BIND 95 102 ATP (POTENTIAL).
 SQ SEQUENCE 742 AA; 84202 MW; 47C40A367BAA77B5 CRC64;
 Query Match 38.1%; Score 642; DB 1; Length 742;
 Best Local Similarity 45.0%; Pred. No. 9.8e-42;
 Matches 150; Conservative 50; Mismatches 117; Indels 16; Gaps 6;
 QY 6 VAVCVVRVPLNSREESLG-ETAQVYKTDNNVIQV-----DGSKSENFDRVFHGHNETT 58
 Db 9 VKVVVRCRPMNSKEISQGHKRVEMDNKRGLEVNTNPKGPPGEPNKSFTFTVYDWSKQ 68
 QY 59 KNVYEELAAPIIDSAIQNGNFIAYGTQASGKTYTMMG---SEDLGVIPRAIHDIKOK 115
 Db 69 IDLYDETFRSLVESVLQGFNGFIAYGTQGTOKFTMEGVRNPELRGVIPNSFHFIFTH 128
 QY 116 IKKFPDFEFLRVSYMEIYNETITLLCGTQMKPLIREDVNRVYVADLTREVVYTSSE 175
 Db 129 IARTQNOQFLVRASYLEIVQEIRDLAKDQK-KELDLKERPDGTGVYKDLSSFTVSKV 187
 QY 176 MALKWITKGEKSRHYGETKMQRSRSHITFRMILESEKGEPSNCEGSKVSHLNLVDL 235
 Db 188 EIEHVTVGNNSRVSSTNMNEHSSRSHAITITIECSLGVG--ENHIVGKLNLDL 245
 QY 236 AGSRAQTGAAGVRLKEGCNINSLFILGQVVKLSGQVGGFINVRDYSKLTILQNSL 295
 Db 246 AGSERQAKTGATGDELKEATKINLSLALGNVISALVDGK--SSHIPYRDSKLTILQNSL 304
 QY 296 GGNPKTRIICITPV--SFDLTLALQFASAK 326
 Db 305 GGNKTVVANNMGPASYNFDETTITTLRYANRAK 337

RESULT 7
 KF4A_MOUSE
 ID KF4A_MOUSE STANDARD; PRT; 1231 AA.
 AC P33174;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chromosome-associated kinesin KIF4A (Chromokinesin).
 GN KIF4A OR KIF4 OR KNS4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE=95014709; PubMed=7929562;

RA Sekine Y., Okada Y., Noda Y., Kondo S., Aizawa H., Takemura R.,
RA Hirokawa N.;
RA "A novel microtubule-based motor protein (KIF4) for organelle
RT transports, whose expression is regulated developmentally";
RL J. Cell Biol. 127:187-201(1994).
RN [2]
RP SEQUENCE OF 91-240 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93077686; PubMed=1447303;
RA Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M.,
RA Hirokawa N.;
RT "Kinesin family in murine central nervous system.";
RL J. Cell Biol. 119:1287-1296(1992).
CC -!- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOLAR
CC SPINDLE STABILIZATION. Nuclear. Associated with mitotic
CC chromosomes.
CC -!- SUBCELLULAR LOCATION: Nuclear. Associated with mitotic
CC chromosomes.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PYRAMIDAL CELLS IN JUVENILE
CC HIPPOCAMPUS, GRANULAR CELLS IN JUVENILE CEREBELLAR CORTEX AND IN
CC ADULT SPLEEN.
CC -!- SIMILARITY: Belongs to the kinesin-like protein family.
CC Chromokinesin subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; D12646; BAA02167.1; -
CC PIR; A54803; A54803.
CC HSSP; P17119; 3KAR.
CC MGD; MGI:108389; Kif4.
CC InterPro; IPR001752; kinesin_motor.
CC Pfam; PF00225; kinesin; 1.
CC PRINTS; PR00380; KINESINHEAVY.
CC SMART; SM00129; KISC; 1.
CC PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
CC PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
CC Motor protein; Microtubule; ATP-binding; DNA-binding;
CC Nuclear protein; Coiled coil.
CC
CC KINESIN-MOTOR.
CC COILED COIL (BY SIMILARITY).
CC DOMAIN 351 1000
CC FT DOMAIN 1001 1231
CC FT NP_BIND 88 95
CC FT CONFLICT 112 112 I -> S (IN REP. 2).
CC FT SEQUENCE 1231 AA; 139551 MW; F34FZC2D21158FE4 CRC64;
CC
CC Query Match 38.0%; Score 641.5; DB 1; Length 1231;
CC Best Local Similarity 44.3%; Pred. No. 2.1e-41;
CC Matches 147; Conservative 53; Mismatches 115; Indels 17; Gaps 7;
CC
CC 6 VAVCVVRPLNGREESLG-ETAQVYKTNVYQVDSKSNFDFVPHGNETTKNVEE 64
CC 10 VRVALRCRPLVSKIEKGCQCLSFVPEQPQV--VGNDSFTYDFDPSTPEQEVNT 67
CC 65 IAAPIITDSALQNGTIFAYGQTASGKTYTMGS---EDH---LGVIPRAIHDFQKIK 117
CC 68 AVAPLTKGVFKGNATVLAGYQTSKTYSMGAYTAQEHDASIGVPRVIQLLFEIN 127
CC 118 KFPDPFLLRVSYMEIYNETITDLCCGT-QKMKPLIREDVNNVYADITVEVYVISEM 176
CC 128 KKSDFEFTLVKSYLEIYNEIILLCSREKATQINREDPKGKIVGLTEKTVLVASD 187
CC 177 ALKWIITKGEKSRHYGTEKMNQSRSHITFRMILESPKEGPNCEGSVVKSHNLVDLA 236
CC 188 TVSCLEQGNNSRTVASTAMNSQSRSHAITFISIEQRK-----NDKNSFRSKLHVDLA 243
CC 237 GSERAAGTGAAGVRLKGCNCNRSFLITGVIVKILSDQGVGFYINRDSKLTILQNSLG 296
CC 244 GSERQKTKAGDKLREGININRGLLCLGNVISAIGDDKGNFVPYRDSKLTLLQDLSLG 303

QY 297 GNPETRIITCTTPV--SPDETITLQFASTAK 326
DB 304 GNSHTLMIACVSPADSNLEETINTLYADRAR 335

RESULT 8
KF3B HUMAN STANDARD; PRT; 747 AA.
ID O15066;
AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kinesin-like protein KIF3B (Microtubule plus end-directed kinesin
DE motor 3B) (HH0048).
DE KIF3B OR KIAA0359.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. VII.
RA The complete sequences of 100 new cDNA clones from brain which can
RA code for large proteins in vitro.";
RA DNA Res. 4:141-150(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Cleghon S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhama P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S.D., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
RN [3]
RP IDENTIFICATION IN A COMPLEX WITH SMC3 AND KIFAP3B.
RX MEDLINE=98175913; PubMed=9506951;
RA Shimizu K., Shirataki H., Honda T., Minami S., Takai Y.;
RT "Complex formation of SNAP/KAP3, a KIF3A/B ATPase motor-associated
RT protein, with a human chromosome-associated polypeptide."
RT J. Biol. Chem. 273:6591-6594(1998).
CC -!- FUNCTION: Involved in tethering the chromosomes to the spindle
CC pole and in chromosome movement. Microtubule-based anterograde
CC translocator for membranous organelles. Plus end-directed
CC microtubule sliding activity in vitro (By similarity).
CC -!- SUBUNIT: Heterodimer of KIF3A and KIF3B (By similarity). Interacts
CC with the SMC3 subunit of the cohesin complex.

```

CC CC      -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC CC      II SUBFAMILY.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC      the European Bioinformatics Institute. There are no restrictions on its
CC CC      use by non-profit institutions as long as its content is in no way
CC CC      modified and this statement is not removed. Usage by and for commercial
CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL: AB002357; BAA20815.1; -
CC CC      EMBL: AL21897; CAC16425.1; -
CC CC      HSPB: P17119; 3KAR.
CC CC      Genew: HGNC:6320; KIF3B.
CC CC      MIM: 603754; -.
CC CC      DR GO: GO:0005873; C:plus-end kinesin complex; TAS.
CC CC      DR GO: GO:0003777; F:microtubule motor activity; TAS.
CC CC      DR GO: GO:0008574; F:plus-end-directed kinesin ATPase activity; TAS.
CC CC      DR GO: GO:0008089; F:anterograde axon cargo transport; TAS.
CC CC      DR GO: GO:0007368; P:determination of left/right asymmetry; TAS.
CC CC      DR InterPro: IPR001752; Kinesin_motor.
CC CC      DR Pfam: PF00225; kinesin_1.
CC CC      DR PRINTS: PR00380; KINESINHEAVY.
CC CC      DR SMART: SM00129; KISC; 1.
CC CC      DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
CC CC      DR PROSITE: PS00667; KINESIN MOTOR DOMAIN2; 1.
CC CC      KW Motor protein; Microtubule; ATP-binding; Coiled coil; Neurone.
CC CC      FT DOMAIN 1 345 KINESIN-MOTOR (BY SIMILARITY).
CC CC      FT DOMAIN 346 579 COILED COIL (BY SIMILARITY).
CC CC      FT NP BIND 580 747 GLOBULAR.
CC CC      FT DOMAIN 96 103 ATP (POTENTIAL).
CC CC      FT DOMAIN 386 393 POLY-GLY.
CC CC      FT DOMAIN 394 406 POLY-GLU.
CC CC      FT DOMAIN 723 730 POLY-SER.
CC CC      SQ SEQUENCE 747 AA; 85125 MW; 97FA4573AFA87023 CRC64;

Query Match
Best Local Similarity 37.4%; Score 631; DB 1; Length 747;
Matches 147; Conservative 54; Mismatches 115; Indels 20; Gaps 7;

QY 5 AVAVCVVRPLNSREESLG-----ETAQVYVKTDDNNVIYQVDGSKSFNDRVPHGN 55
Db 9 SVRVVVRCPWNGKEKAASVDVVDVKLGQVSVKPKGTSHM--PKTFTFDAVDWN 66
QY 56 ETKNVYEEIAPIIDSAIQYNGTIFAYGQTASGKTYTM---MGSEDLGLGVIPRAIHDI 112
Db 67 AKQFELYDETFRPLVDVSVLQGFNGTIFAYGQTGKTGTYTMGIRGDPKRGVIPSFDHI 126
QY 113 FQKIKKFPDRFELLRVSYMEIYNETITDLCGTQKMKPLIIRDVNRNVYADLTSEVVY 172
Db 127 FTHISRSQOQYLVRASYLEIYQEEIRDLDSKQ--TKRLELKERPDGTGVYVKDLSFFVK 185
QY 173 TSEMALKWITTKGKSRHYGTEKMNORSSRSHITFRMILESREKGEPSNCGSVKSHLNL 232
Db 186 SVKEIEHVMVNGNQNSVGATNMHSHSRSHAFVITIECEVSG--LDGENHIRVGKLN 243
QY 233 VDLAGSRAAQTGAAGVRLKEGCNINRSLIFILGQVVKKLSGQGVGFNYRDSKLTLQ 292
Db 244 VDLAGSERQAQTGAQGERLKEATKINLSLALGNVVISALVDGK--STHPIYRDSKLTLQ 302
QY 293 NSLGGNPKTRICHTITVSPF--DETFLALQFASAK 326
Db 303 DSLGGNKTVMVANGFASVNVETLTITRYANRAK 338

RESULT 9
KF3B_MOUSE
ID_KF3B_MOUSE
AC Q61771;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

```

DE DE      Kinesin-like protein KIF3B (Microtubule plus end-directed kinesin
DE DE      motor 3B).
DE GN KIF3B.
DE OS Mus musculus (Mouse).
DE OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DE CX NCBI_TaxID=10090;
DE RN [1]
DE RP SEQUENCE FROM N.A.
DE RC STRAIN=ICR; TISSUE=Brain;
DE RX MEDLINE=96032268; PubMed=7559760;
DE RA Yamazaki H., Nakata T., Okada Y., Hirokawa N.;
DE RT "KIF3B/B: a heterodimeric kinesin superfamily protein that works as a
DE RT microtubule plus end-directed motor for membrane organelle
DE RT transport.";
DE RL J. Cell Biol. 130:1387-1399(1995).
DE CC -!- FUNCTION: Involved in tethering the chromosomes to the spindle
DE CC pole and in chromosome movement. Microtubule-based anterograde
DE CC translocator for membranous organelles. Plus end-directed
DE CC microtubule sliding activity in vitro (By similarity).
DE CC -!- SUBUNIT: Interacts with the SMC3 subunit of the cohesin
DE CC complex (By similarity). Heterodimer of KIF3A and KIF3B.
DE CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
DE CC II SUBFAMILY.
DE CC -----
DE CC This SWISS-PROT entry is copyright. It is produced through a collaboration
DE CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
DE CC the European Bioinformatics Institute. There are no restrictions on its
DE CC use by non-profit institutions as long as its content is in no way
DE CC modified and this statement is not removed. Usage by and for commercial
DE CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
DE CC or send an email to license@isb-sib.ch).
DE CC -----
DE CC EMBL: D26077; BAA05070.1; -.
DE DR PIR: A57107; A57107.
DE DR HSPB: P17119; 3KAR.
DE DR MGD: MGI:107688; Kif3b.
DE DR InterPro: IPR001752; kinesin_motor.
DE DR Pfam: PF00225; kinesin_1.
DE DR PRINTS: PR00380; KINESINHEAVY.
DE DR SMART: SM00129; KISC; 1.
DE DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
DE DR PROSITE: PS00667; KINESIN MOTOR DOMAIN2; 1.
DE KW Motor protein; Microtubule; ATP-binding; Coiled coil; Neurone.
DE FT DOMAIN 1 345 KINESIN-MOTOR (BY SIMILARITY).
DE FT DOMAIN 346 579 COILED COIL (BY SIMILARITY).
DE FT NP BIND 580 747 GLOBULAR.
DE FT DOMAIN 96 103 ATP (POTENTIAL).
DE FT DOMAIN 386 393 POLY-GLY.
DE FT DOMAIN 394 406 POLY-SER.
DE FT DOMAIN 723 730 POLY-SER.
DE SQ SEQUENCE 747 AA; 85288 MW; FA369A4190ECB47 CRC64;

Query Match
Best Local Similarity 37.4%; Score 630; DB 1; Length 747;
Matches 147; Conservative 54; Mismatches 115; Indels 20; Gaps 7;

QY 5 AVAVCVVRPLNSREESLG-----ETAQVYVKTDDNNVIYQVDGSKSFNDRVPHGN 55
Db 9 SVRVVVRCPWNGKEKAASVDVVDVKLGQVSVKPKGTSHM--PKTFTFDAVDWN 66
QY 56 ETKNVYEEIAPIIDSAIQYNGTIFAYGQTASGKTYTM---MGSEDLGLGVIPRAIHDI 112
Db 67 AKQFELYDETFRPLVDVSVLQGFNGTIFAYGQTGKTGTYTMGIRGDPKRGVIPSFDHI 126
QY 113 FQKIKKFPDRFELLRVSYMEIYNETITDLCGTQKMKPLIIRDVNRNVYADLTSEVVY 172
Db 127 FTHISRSQOQYLVRASYLEIYQEEIRDLDSKQ--TKRLELKERPDGTGVYVKDLSFFVK 185
QY 173 TSEMALKWITTKGKSRHYGTEKMNORSSRSHITFRMILESREKGEPSNCGSVKSHLNL 232
Db 186 SVKEIEHVMVNGNQNSVGATNMHSHSRSHAFVITIECEVSG--LDGENHIRVGKLN 243

```

QY 233 VDLGASERAAQTGAAGVRLKEGCNINRSILFGLQVVKLSGQVGFNRYRDSKLTIRLQ 292
 Db 244 VDLGASERAAQTGAAGVRLKEGCNINRSILFGLQVVKLSGQVGFNRYRDSKLTIRLQ 302
 QY 293 NSLGNPKTRITCTIPVNSF--DETALQFASAK 326
 Db 303 DSLGGNAKTMVANVPASYNVEETLTTLRYANRAK 338

RESULT 10
 ID KF4A XENLA STANDARD; PRT; 1226 AA.
 AC Q91784; Q9PS10;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chromosome-associated kinesin KLP1 (Chromokinesin).
 GN KLP1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN NCBI_TaxID=8355;
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Oocyte;
 RX MEDLINE=95236444; PubMed=7720067;
 RA Vernos I., Raats J., Hirano T., Heasman J., Karsenti E., Wylie C.;
 RT "Xklp1, a chromosomal Xenopus kinesin-like protein essential for spindle organization and chromosome positioning.";
 RL Cell 81:117-127(1995).
 RN [2]
 RP SEQUENCE OF 9-338 FROM N.A.
 RX MEDLINE=93246065; PubMed=8482413;
 RA Vernos I., Heasman J., Wylie C.;
 RT "Multiple kinesin-like transcripts in Xenopus oocytes.";
 RL Dev. Biol. 157:232-239(1993).
 CC -!- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOLAR
 CC -!- SPINDLE STABILIZATION.
 CC -!- SUBCELLULAR LOCATION: Nuclear. Associated with mitotic chromosomes.
 CC -!- TISSUE SPECIFICITY: Expressed in oocytes, eggs, testes and brain.
 CC -!- SIMILARITY: Belongs to the kinesin-like protein family.
 CC Chromokinesin subfamily.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 DR EMBL; X82012; CAA57539.1; -;
 DR PIR; I51617; I51617.
 DR HSSP; P17119; 3KAR.
 DR InterPro; IPR001752; kinesin_motor.
 DR PRINTS; PF00225; kinesin; 1.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; P500411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; P50067; KINESIN MOTOR DOMAIN2; 1.
 KW Motor protein; Microtubule; ATP-binding; DNA-binding;
 KW Nuclear protein; Coiled coil.
 FT DOMAIN 1 350 KINESIN-MOTOR.
 FT DOMAIN 351 1006 COILED COIL (BY SIMILARITY).
 FT DOMAIN 1007 1226 GLOBULAR.
 FT NP BLND 87 94 I -> L (IN POTENTIAL).
 FT CONFLICT 163 163 I -> L (IN REF. 2).
 SQ SEQUENCE 1226 AA; 138923 MW; 7F0275FCF3316697 CRC64;

Query Match 37.3%; Score 628.5; DB 1; Length 1226;
 Best Local Similarity 44.1%; Pred. No. 2.1e-40;
 Matches 149; Conservative 53; Mismatches 117; Indels 19; Gaps 9;
 QY 2 EGG-AVAVCVRVPLNSREESLG-ETAQVYWKTDNNVIVQVDGSKSFNDRFVHGNETTK 59
 Db 4 DEGIPIRVVALRCPLVPKENNEGKCMCLTFVPEQOVI--VGTEKFTYDYVDFPSAEQ 61
 QY 60 NYEEIAAPLIDSAIQVNGTIFAYGQTASGKTYTMMGSEDH-----LGVIPRAHDI 112
 Db 62 EVYNSAVAPLIKGLFKGYNAVLAVGOTSGKTYSGGAYTHNQENPTVGVIPRTVIAL 121
 QY 113 FQIKKFPDPREFLLRVSYMEINTEITDLL-CQTQMKPLIIFEDVNRNVYVADLTVEEV 171
 Db 122 FREIHQRPWEFNLKVSYLEIYNEEILDLIYAARDKNTISIREDEKPKIKICGLTERDV 181
 QY 172 YTSEMALKWITKEKSRHYGETKNQORSSRSHTIFRMILESRKBPSPNCEGSKVSHLN 231
 Db 182 KTAIDLTSLCLEQGNSSRTVASTAMNSQSSRSHAFITISIEQRKEGKNN--SFR-SKLH 237
 QY 232 LVDLGASERAAQTGAAGVRLKEGCNINRSILFGLQVVKLSGQVGFNRYRDSKLTIRI 290
 Db 238 LVDLGASERAAQTGAAGVRLKEGCNINRSILFGLQVVKLSGQVGFNRYRDSKLTIRI 297
 QY 291 LQNSLGNPKTRITCTIPV--SFDETALQFASAK 326
 Db 298 LQNSLGNPKTRITCTIPV--SFDETALQFASAK 326

RESULT 11
 ID KF17 HUMAN STANDARD; PRT; 1029 AA.
 AC Q9P2E2; Q95077; Q8N411;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kinesin-like protein KIF17 (KIF3-related motor protein).
 GN KIF17 OR KIF3X OR KIAA1405.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimberley A., White S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 78-1029 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Ohara O., Nagase T., Kikuno R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 239-1029 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 RN [4]
 RP SEQUENCE OF 618-1029 FROM N.A. (ISOFORM 2).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Udwin T.B., Toshiyuki S., Abramson R.D., Mullany S.J., Raha S.S., Loughran N.A., Peters G.J., McKernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

DR	GO:	GO:0005871;	C:kinesin complex; IDA.
DR	GO:	GO:0003777;	F:microtubule motor activity; IDA.
DR	GO:	GO:0005515;	F:protein binding; IPI.
DR	GO:	GO:0007017;	P:microtubule-based process; IDA.
GO:	GO:	GO:0016192;	P:vessicle-mediated transport; IDA.
DR	InterPro:	IPR001752;	kinesin_motor.
DR	Pfam:	PF00225;	kinesin; 1.
DR	PRINTS:	PR00380;	KINESINHEAVY.
DR	SMART:	SM00129;	KISG; 1.
DR	PROSITE:	PS00411;	KINESIN MOTOR DOMAIN1; 1.
DR	PROSITE:	PS00677;	KINESIN MOTOR DOMAIN2; 1.
KW	Motor protein:	Microtubule;	Atp-binding; Coiled coil; Transport;
KW	Protein transport:		
FT	DOMAIN	1	265 KINESIN-MOTOR.
FT	DOMAIN	346	470 COILED COIL (POTENTIAL).
FT	DOMAIN	748	855 COILED COIL (POTENTIAL).
FT	NP BIND	91	98 ATP (POTENTIAL).
SQ	SEQUENCE	1038 AA;	116372 MW; 2BED852A3AFD8D46 CRC64;
 Query Match 36.4%; Score 613.5; DB 1; Length 1038;			
Best Local Similarity 42.3%; Pred.No.2.4e-39;			
Matches 142; Conservative 57; Mismatches 116; Indels 21; Gaps 8			
QY	5	AVAVCVVRPLNSRESISLG-ETAQVYWKTDNNVIYQVDGS-----KGFNFDRVPHGNETT 58	
DB	5	SVKVVRCPMKNREELSCQSVVTDSARGCQFIQNPGAADPPKQFTFDGAYYIEHFT 64	
QY	59	KNVYEIIAAPIIDSAIQNGYTIIFAYGTQASGYITMMGSD--HLGVIPRAIHDIFOK 115	
DB	65	EQLYNEIAVPLVEGVTEGNYTIFAYGTQSGKSFTMQGLDPQCQRGIILPRAFEHVFS 122	
QY	116	IKKFPDELLAVSYMEIVNETITDLGGTQMKEPLIIRVDNRNVIYVAADLTEEVYTSE 179	
DB	125	VQAENTKFLVASYLEIYNEDVHOLL-GADTKQRLLEKEHPKGVIYVKLSMTHVNVA 181	
QY	176	MALKWTITKEKSRHYGETVMONRSRSHTIPRMILE---SREKGPSPNCESGVKVSUHLN 233	
DB	184	OQERVMTGWKNRANGVITLMNKDDSSKSHSIFTNIEIYAVDERG----KOHLRAGKLNL 233	
QY	233	VDLAGSERAAQTGAAGVRLKEGNIINRSIFIQVKKLSQGVGGFINYRDSKLTRIQQ 299	
DB	239	VDLAGSERSOKTGATGERLKEATKINLSLSALGNVISALVDGRG-KHIPYRDSKLTRIQQ 299	
QY	293	NSLGGPKPTFICTTPV--SPDETTLAQFASTAK 326	
DB	298	DSLGGNTKLWLVAACLSPADNNYDELSTLYANRAK 333	
 RESULT 14			
ID	KF4A_CHICK	STANDARD;	PRT; 1225 AA.
AC	Q90640; Q90608;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Chromosome-associated kinesin KIF4A (Chromokinesin).		
GN	KIF4A.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE		
RP	SPECIFICITY.		
RC	STRAIN=White leghorn; TISSUE=Embryonic retina;		
RX	MEDLINE=95181533; PubMed=7876303;		
RA	Wang S.Z.; Adler R.		
RT	"Chromokinesin: a DNA-binding, kinesin-like nuclear protein.";		
RL	J. Cell Biol. 128:761-768(1995).		
RL	[2]		
RP	SEQUENCE OF 728-1088 FROM N.A.		
RP	STRAIN=White leghorn; TISSUE=Embryonic retina;		
RC			

DR	GO: 0005871; C:kinesin complex; IDA.	
DR	GO: 00003777; F: microtubule motor activity; IDA.	
DR	GO: 00005515; F: protein binding; IPI.	
DR	GO: 00007017; P: microtubule-based process; IDA.	
DR	GO: 00016192; P: vesicle-mediated transport; IDA.	
DR	InterPro: IPR001752; kinesin_motor.	
DR	Pfam: PF00225; kinesin; 1.	
DR	PRINTS: PR00380; KINESINHEAVY.	
DR	SMART: SM00129; KISG; 1.	
DR	PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.	
DR	PROSITE: PS0067; KINESIN MOTOR DOMAIN2; 1.	
KW	Motor protein; Microtubule; ATP-binding; Coiled coil; Transport;	
KW	Protein transport.	
FT	DOMAIN 1 265 KINESIN-MOTOR	
FT	DOMAIN 346 470 COILED COIL (POTENTIAL).	
FT	DOMAIN 748 855 COILED COIL (POTENTIAL).	
FT	NP BIND 91 98 ATP (POTENTIAL).	
SEQUENCE	1038 AA; 116372 MW; 2BED852A3AFD8D46 CRC64;	
Query Match	36.4%; Score 613.5; DB 1; Length 1038;	
Best Local Similarity	42.3%; Pred. No. 2.4e-39;	
Matches 142; Conservative	57; Mismatches 116; Indels 21; Gaps	
QY	5 AVAVCVVRPLNSRESISLG-ETAQYVWKTDNNVYQVDGS-----KGFNFDVRVPHGNETT 58	
DB	5 SVKVVVRCPMKRERELSCQSVVTVDSARGCQFIQNPGAADPPKQFTFDGAYYIEHFT 64	
QY	59 KNVYEIIAIPIDSAIQVNGTIFPAYGQTASGKYITWMSGD---HLGVIPRAIHDIFOK 115	
DB	65 EQIYNEIAYPLVEGVTEGNGTIFPAYGQTSGKSTMQGLDPPCQCGIILPRAFEHFES 128	
QY	116 IKKFPDRELLAVSYMEIYNETITDLGCTQMKPLIIRVDNRNVYVADLTEEVVYTSE 179	
DB	125 VQCAENTKFLVASYLDIENVDHOLL-GADTKQRLKLEKHEPKGVYKGLSMHTVHVA 181	
QY	176 MALKWTIKCEKSRHYGETKWNORSRSRSHITFRMILE---SREKGPSPNCESGVKVSHLN 231	
DB	184 QCRVMEYTKGNRAVGYTLNMKDDSRKSHSIFTNIEIYAVDERG----KQHLRAGKLN 239	
QY	233 VLIAGSERAQCTGAAGVRLKEGNNINRSFIIGVVKLSQGVGGFINYRDSKLTRLIQ 291	
DB	239 VDLAGSERSOKTGATGERLKEATKINLSALGNVISALVDGRC-KHPIYRDSKLTRLIQ 299	
QY	293 NSLGGNPKPHIICITTPV--SPDETALQFASTAK 326	
DB	298 DSIIGGNTKLWVACLSPADNNYDEILSTLYANRAK 333	
RESULT 14		
KF4A_CHICK		
ID	KF4A_CHICK STANDARD; PRT; 1225 AA.	
AC	Q90640; Q90608;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Chromosome-associated kinesin KIF4A (Chromokinesin).	
GN	KIF4A.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE	
RP	SPECIFICITY.	
RC	STRAIN=White leghorn; TISSUE=Embryonic retina;	
RX	MEDLINE=95181533; PubMed=7876303;	
RA	Wang S.Z., Adler R.	
RT	"Chromokinesin: a DNA-binding, kinesin-like nuclear protein.";	
RL	J. Cell Biol. 128:761-768(1995).	
RL	[2]	
RP	SEQUENCE OF 728-1088 FROM N.A.	
RP	STRAIN=White leghorn; TISSUE=Embryonic retina;	
RC		

```

RX MEDLINE=94151328; PubMed=8108415;
RA Wang S.Z., Adler R.;
RT "A developmentally regulated basic-leucine zipper-like gene and its
RL expression in embryonic retina and lens.";
Proc. Natl. Acad. Sci. U.S.A. 91:1351-1355 (1994).
CC -!- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOLAR
CC SPINDLE STABILIZATION.
CC -!- SUBCELLULAR LOCATION: Nuclear. Associated with mitotic
CC chromosomes.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PROLIFERATING CELLS;
CC NEUROEPITHELIUM OF EMBRYOS.
CC -!- SIMILARITY: Belongs to the kinesin-like protein family.
CC Chromokinesin subfamily.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; U18309; AAC59666.1; -.
DR EMBL; U04821; AAA18960.1; -.
DR PIR; A56514; A56514.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW Motor protein; Microtubule; ATP-binding; DNA-binding;
Nuclear protein; Coiled coil.
FT DOMAIN 1 351 KINESIN-MOTOR.
FT DOMAIN 352 1003 COILED COIL (BY SIMILARITY).
FT DOMAIN 1004 1225 GLOBULAR.
FT NP_BIND 98 95
FT NP_BIND 1087 1088 ATP (POTENTIAL).
FT CONFLICT 1087 1088 KG -> RI (IN REF. 2).
SQ SEQUENCE 1225 AA; 138923 MW; FA01ED83425F5875 CRC64;
-----
Query Match 36.1%; Score 608; DB 1; Length 1225;
Best Local Similarity 42.4%; Pred. No. 38-39;
Matches 143; Conservative 58; Mismatches 118; Indels 18; Gaps 8;
QY 2 BEGAVAVCVRVPLNSREESLG-ETAQVYVKKTDNNVIVQVDSKGFNDFVPHGNETKN 60
Db 6 EKGIPVRVRCRPLVPKETSQCWCLSFVPGEPQVI--VGSDKAFTYDYVDFDPSVEQEE 63
QY 61 VVEETAAPIDSATQGYNGTIFAYQGTASGKTYTMMG----SEDR---LGVIPRAIHDF 113
Db 64 VNTAVAPLRIGIFKGYNATVLAQGTSKGYTSMGGTYTASQEHDPMSGVIPRVIKLLF 123
QY 114 QKIKKFPDREELLRVSYMEIYNETITDLCGT-QKMKPLIIREDVNRNVYADLTVEVY 172
Db 124 KEKQRQDWEFVLKVSLEYIETNEDILLDCSSRRSSQISIREDPKEGIRVGLTERVA 183
QY 173 TSEMALKWITKGEKSRHYGETKMNQSRSSHTIFRMILESEKGEPSKCVKVSHLN 232
Db 184 SARDTVSCLEGNNCRVTASTAMNSQSSRSHTAFTICIDQKK-----NDKMSFSHKLHL 239
QY 233 VDLAGSERAATGAGVRLKEGCNINSLFLTGQVKKL-SDGVGGFVINYRDSKLTRIL 291
Db 240 VDLAGSERQKTKAEGRLKEGININRGLLCLGNVISAIGENKKGGFVPRYDSKLTRLL 299
QY 292 QNSLGGNPKTKIITTPV--SEDETALOPASTAK 326
Db 300 QDSLGGNSHTLMIACVSPADSNLETLNTRYADR 336
-----
RESULT 15
OSM3_CABEL STANDARD; PRT; 672 AA.
ID -OSM3_CABEL

```

```

P46873;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Kinesin-like protein osm-3.
OSM-3.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=95230679; PubMed=7714894;
Tabish M., Siddiqui Z.K., Nishikawa K., Siddiqui S.S.;
"Exclusive expression of C. elegans osm-3 kinesin gene in
chemosensory neurons open to the external environment.";
J. Mol. Biol. 247:377-389 (1995).
[2]
PRELIMINARY SEQUENCE OF 1-397 FROM N.A.
STRAIN=Bristol N2;
MEDLINE=93379214; PubMed=7690265;
Shakir M.A., Fukuehige T., Yasuda H., Miwa J., Siddiqui S.S.;
"C. elegans osm-3 gene mediating osmotic avoidance behaviour encodes
a kinesin-like protein.";
NeuroReport 4:891-894 (1993).
-!- TISSUE SPECIFICITY: AMPHID AND IL2 NEURONS.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC II SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; D38632; BAA07612.1; -.
DR EMBL; D14968; BAA20996.1; -.
DR PIR; S54351; S54351.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW Motor protein; Microtubule; ATP-binding; Coiled coil.
FT DOMAIN 57 300 KINESIN-MOTOR.
FT NP_BIND 461 497 COILED COIL (POTENTIAL).
FT NP_BIND 130 137 ATP (POTENTIAL).
SQ SEQUENCE 672 AA; 75456 MW; 4E2160F7042AFCD7 CRC64;
-----
Query Match 35.9%; Score 605; DB 1; Length 672;
Best Local Similarity 46.9%; Pred. No. 6e-39;
Matches 137; Conservative 47; Mismatches 94; Indels 14; Gaps 6;
QY 41 DG-SKSFNFRVFHGNETTKNVVEEIAAPIDSALQCYNGTIFAYQGTASGKTYTMMGE 99
Db 85 DGAAKDTDFGAFVMPRPGQIVNDIVFPLVENVIEGTVFAYGQTSKGTSMQIE 144
QY 100 D---HLGVIPIRAIHDIFQKIKKFPDREELLRVSYMEIYNETITDLCGTQKMKPLIRED 156
Db 145 TIPAQRGVIPRAFDHIFTATATTENVKVLVHCYSLEYINEVEVDLLGADNKKQ-LEIQE 203
QY 157 VNRNVYADLTVEVYVTSSEALKWITKGEKSRHYGETKMNQSRSSHTIFRMILESEK 216
Db 204 PDRGVYVAGLSMEVCHDVPAKELMTRGFNNRHVGATLMNKDSSRSHSITFVVVEGITE- 262
QY 217 EPSNCEGSKVSHNLVDLAGSERAATGAGVRLKEGCNINSLFLTGQVKKLSDGV 276
Db 263 -----TGSIRMGKLNLDLAGSERQSKTGATGRLKEATKINLSLALGNVISALVDGK- 316

```

us-10-045-631b-88_copy_2_329.rsp

Mon Aug 9 11:02:49 2004

QY 277 GGFINYRDSKLTIRILONSLGGNPKTRIICTITPVS--FDETLTALQFASTAK 326
DB 317 SKHIPYRDSKLTIRILQDSLGGNPKTITMIACVSPSSDNYDETLTLLRYANRAK 368

Search completed: July 29, 2004, 09:36:13
JOB time : 4.15048 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 09:27:31 ; Search time 13.9321 Seconds
(without alignments)
7428.155 Million cell updates/sec

Title: US-10-045-631b-88_COPY_2_329

Perfect score: 1686

Sequence: 1 AEGAVACVVRPLNSREE.....PVSFDETLALQFASTAKYM 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1485	88.1	549	11 Q7TPX4	Q7tpx4 mus musculu
2	1258.5	74.6	2954	13 Q42263	Q42263 xenopus lae
3	773.5	45.9	807	10 Q94HV9	Q94hv9 arabidopsis
4	773.5	45.9	823	10 Q957P3	Q957p3 arabidopsis
5	744.5	44.2	459	10 Q9SS30	Q9ss30 arabidopsis
6	738	43.8	888	10 Q9LQ62	Q9lq62 arabidopsis
7	719	42.6	1885	5 Q869B8	Q869b8 dictyosteli
8	707	41.9	160	11 Q35059	Q35059 mus musculu
9	688	40.8	2213	5 Q9VK10	Q9vk10 drosophila
10	688	40.8	2244	5 Q9NCGO	Q9ncgo drosophila
11	683	40.5	1055	10 Q8RWM4	Q8rwm4 arabidopsis
12	683	40.5	1055	10 Q8W5R5	Q8w5r5 arabidopsis
13	673	39.9	1058	10 Q9SUJ0	Q9suj0 arabidopsis
14	667.5	39.6	1033	10 Q9LHL9	Q9lhl9 arabidopsis
15	663.5	39.4	1459	3 P87198	P87198 ustilago ma
16	656	38.9	890	10 Q8W5R6	Q8w5r6 arabidopsis

17	654.5	38.8	954	10 Q9AWM8	Q9awm8 oryza sativ
18	652	38.7	699	5 Q8MPT8	Q8mpt8 caenorhabdi
19	649	38.5	959	10 Q8S950	Q8s950 nicotiana t
20	646.5	38.3	956	10 Q9C7B9	Q9c7b9 arabidopsis
21	644	38.2	408	4 Q8IWH8	Q8iwh8 homo sapien
22	643	38.1	408	11 Q80UK1	Q80uk1 mus musculu
23	643	38.1	443	11 Q8CGJ1	Q8cgj1 mus musculu
24	643	38.1	671	4 Q86XX7	Q86xx7 homo sapien
25	643	38.1	701	11 Q7TSZ7	Q7tsz7 mus musculu
26	643	38.1	1127	4 Q86TN3	Q86tn3 homo sapien
27	641.5	38.0	819	11 Q7TQG6	Q7tqg6 mus musculu
28	641.5	38.0	997	10 Q8FG03	Q8f903 arabidopsis
29	641.5	38.0	1231	11 Q80YP3	Q80yp3 mus musculu
30	639	37.9	699	13 Q98T11	Q98t11 xenopus lae
31	635.5	37.7	735	5 Q9UUD5	Q9u0d5 tetrahymena
32	631.5	37.5	974	10 Q8S905	Q8s905 arabidopsis
33	630.5	37.4	909	10 Q9X103	Q9x103 arabidopsis
34	630	37.4	747	11 Q8BNH4	Q8bnh4 mus musculu
35	630	37.4	757	11 Q8OU27	Q8ou27 mus musculu
36	629.5	37.3	836	5 Q7YUC7	Q7yuc7 tetrahymena
37	629.5	37.3	1193	10 Q7X7H8	Q7x7h8 oryza sativ
38	627.5	37.2	677	5 Q9VRK9	Q9vrk9 drosophila
39	621	36.8	932	10 Q9LXL3	Q9lxl3 arabidopsis
40	621	36.8	937	10 Q8LGU3	Q8lgu3 arabidopsis
41	621	36.8	937	10 Q8L5J2	Q8l5j2 arabidopsis
42	621	36.8	938	10 Q8LNZ2	Q8lnz2 arabidopsis
43	618.5	36.7	1121	10 Q9SVI8	Q9svi8 arabidopsis
44	617	36.6	671	5 Q8MPT7	Q8mpt7 caenorhabdi
45	617	36.6	672	5 Q9GV93	Q9gv93 caenorhabdi

ALIGNMENTS

RESULT 1

Q7TPX4 PRELIMINARY; PRT; 549 AA.

AC Q7TPX4;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Egg;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Egg;

Strausberg R.; RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. DR EMBL, BC052843; AAHS52843.1; -. KW Hypothetical protein. FT NON_TER 549 549 SQ SEQUENCE 549 AA; 62899 MW; B707C97DC9FB3BD3 CRC64;		Best Local Similarity 73.4%; Pred. No. 3.2e-90; Matches 243; Conservative 40; Mismatches 43; Indels 5; Gaps 2;	
Query Match Best Local Similarity 87.8%; Pred. No. 3.2e-109; Matches 288; Conservative 11; Mismatches 29; Indels 0; Gaps 0;			
QY	1 AEEGAVAVCVVRPLNSREESLGETAQVYWKTDNNVIYQVDGSKSFNDRVFHGNETTKN 60		
Db	2 SEGDAVKVCVRPLIQREQ--GDOANLQWKAGNNTISQVDGKTSFNFDRVNSHSTSQ 59		
QY	61 VVEETAAPIIDSAIQYNGTIFAYGQTASGKTYTMMGSDHLGVI PRAIHDFQKIKKFP 120		
Db	60 IYQETAVPIIRALQYNGTIFAYGQTSSGKTYTMMGTNSLGIIPQAIQEVFKIQEIP 119		
QY	121 DREFLLRVSYMEIYNETITDLLCGTQMKPLIREDVNRNVYVADLT EEVVYTSMAWK 180		
Db	120 NREFLLRVSYMEIYNETVKKLDCDRKKKPLETREDFNRVYVADLT EELVMVPVHVIOW 179		
QY	181 IYKGEKSRHYGETMQRSSRSHITFRMILESRKGEPS--NCEGSKVSVSHLNLVDLAG 237		
Db	180 IKKGEKNRYGETMQRSSRSHITFRMILESDRNDPTNSENCDAVAVSHLNLVDLAG 239		
QY	238 SERAAGTGAAGVRLKGCNINRSLFILGQVKKLSGQVGGFINYRDSKLTILQNSLGG 297		
Db	240 SERASQTGAEGVRLKGCNINRSLFILGQVKKLSGQAGGFINYRDSKLTILQNSLGG 299		
QY	298 NPKTRIICTITPVSFDETLTALQFASTAKYM 328		
Db	300 NAKTVIICTITPVSFDETLTALQFASTAKHV 330		
RESULT 3			
Q94HV9	PRELIMINARY; PRT; 807 AA.		
ID	Q94HV9		
AC	094HV9		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Kinesin motor protein (kin2), putative.		
GN	T4M14.11.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Columbia;		
RA	Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,		
RA	Tallon L.J., Rooney T., Uterback T.R., VarAken S.E., Feldblyum T.V.,		
RA	White O., Fraser C.M.;		
RT	"Arabidopsis thaliana chromosome 1 BAC T4M14 genomic sequence.";		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AC027036; AAK62792.1; -.		
DR	GO; GO:0005871; C:kinesin complex; IEA.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0003774; F:motor activity; IEA.		
DR	GO; GO:0007017; P:microtubule-based process; IEA.		
DR	InterPro; IPR001752; kinesin_motor.		
DR	Pfam; PF00225; kinesin; 1.		
DR	PRINTS; PR00380; KINESINHEAVY.		
DR	SMART; SM00129; KISC; 1.		
DR	PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.		
DR	PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.		
SQ	SEQUENCE 807 AA; 91260 MW; FD7CDAD68EA30C28 CRC64;		
Query Match		45.9%; Score 773.5; DB 10; Length 807;	
Best Local Similarity		52.0%; Pred. No. 1.5e-52;	
Matches 173; Conservative		46; Mismatches 89; Indels 25; Gaps 7;	
QY	6 VAVCVVRPLNSREESLGETAQVYWKTDNNVIYQVDGSKSFN-----FDRVFHGN 56		
Db	4 ICVAVVRP-----PAPENGASLWKVEDN---RISLHSLDPTTTTASHAFHVDPESS 54		
QY	57 TTKNYVEETAAPILDSAIQYNGTIFAYGQTASGKTYTMMGSDHLGVI PRAIHDFQKI 116		

```

Db      55 TNASVYELLTKDIIHAAVEGNGTAFAYGQTSSGKTTMTGSETDPGIIIRSRVDVFERI 114
QY      117 KFPDPREFLRVSMEIYNETITDLCGTQMKPLIIREDVNRNVYVADLTETEEVVYTTSEM 176
Db      115 HMTSDREFLRVSMEIYNEEINDLL--AVENQLQIHEHLERGCVFVAGLKEEIVSDAEQ 172
QY      177 ALKWIITGKESRHYGETKMNQSRSHITFRMILESEKGEPCNCEGSKVSHNLNLDLA 236
Db      173 ILKLDSGEVNRHFGETNMNVHSRSHITFRMVIESR--GKDNSSSDAIRVSVLNLVDLA 230
QY      237 GSERAQTGAAGVRLKEGNCNINSLFLGQVIVKLSDG--QVGGFINVRDSDKSLRILQNSL 295
Db      231 GSRIAKTGAGVRLQEGKYINKSLMLGNVINKLSDTKLRAHIPYRDSKLRILQPAL 290
QY      296 GGNPKTRIITCTIPVS--FDETLTALQFASTAK 326
Db      291 GGNAKTCTIITIAPEEHIEESKGTILQFASRAK 323

RESULT 4
Q9S7P3
ID Q9S7P3 PRELIMINARY; PRT; 823 AA.
AC Q9S7P3;
DT 01-MAY-2000 (trEMBLrel. 13, Created)
DT 01-MAY-2000 (trEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (trEMBLrel. 25, Last annotation update)
DE Kinesin-like protein.
GN ZCFI25.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Ooe H., Kato A., Komeda Y.;
RT "Arabidopsis thaliana genomic sequence for a kinesin-like protein.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kato A., Suzuki M., Kuwahara A., Ooe H., Higano-Inaba K., Komeda Y.;
RT "Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana
RT genomic region located around the 100 map unit of chromosome 1.";
RL Gene 239:309-316(1999).
DR EMBL; AB028470; BAA88114.1; -
DR EMBL; AB028468; BAA88112.1; -
DR PIR; T52425; T52425.
DR HSRF; P33176; IBC2.
DR GO; GO:0005871; C:kinesin complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR001752; P:microtubule-based process; IEA.
DR Pfam; PF00225; kinesin_1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
SQ SEQUENCE 823 AA; 93148 MW; 6AFB1C622E4632C9 CRC64;

Query Match 45.9%; Score 773.5; DB 10; Length 823;
Best Local Similarity 52.0%; Pred. No. 1.5e-52;
Matches 173; Conservative 46; Mismatches 89; Indels 25; Gaps 7;

QY      6 VAVCVVRPLNRSREESIGETAQVYWKTDNNVIYQVDSKSFN-----FDRVFHNE 56
Db      4 ICVAVRVP-----PAPENGASLWKVEDN--RISLHSLDITTTASHAFDHFVDESS 54
QY      57 TTKNVYEIAPIIDSALIOGNGTIFAYGQTASGKTYTMGSEDLGVIPRAIHFOKI 116

```

```

Db      55 TNASVYELLTKDIIHAAVEGNGTAFAYGQTSSGKTTMTGSETDPGIIIRSRVDVFERI 114
QY      117 KFPDPREFLRVSMEIYNETITDLCGTQMKPLIIREDVNRNVYVADLTETEEVVYTTSEM 176
Db      115 HMTSDREFLRVSMEIYNEEINDLL--AVENQLQIHEHLERGCVFVAGLKEEIVSDAEQ 172
QY      177 ALKWIITGKESRHYGETKMNQSRSHITFRMILESEKGEPCNCEGSKVSHNLNLDLA 236
Db      173 ILKLDSGEVNRHFGETNMNVHSRSHITFRMVIESR--GKDNSSSDAIRVSVLNLVDLA 230
QY      237 GSERAQTGAAGVRLKEGNCNINSLFLGQVIVKLSDG--QVGGFINVRDSDKSLRILQNSL 295
Db      231 GSRIAKTGAGVRLQEGKYINKSLMLGNVINKLSDTKLRAHIPYRDSKLRILQPAL 290
QY      296 GGNPKTRIITCTIPVS--FDETLTALQFASTAK 326
Db      291 GGNAKTCTIITIAPEEHIEESKGTILQFASRAK 323

RESULT 5
Q9S830
ID Q9S830 PRELIMINARY; PRT; 459 AA.
AC Q9S830;
DT 01-MAY-2000 (trEMBLrel. 13, Created)
DT 01-MAY-2000 (trEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (trEMBLrel. 25, Last annotation update)
DE Putative kinesin-like centromere protein.
GN F14P13.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F14P13 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009400; AAF02823.1; -
DR HSSP; P33176; IBC2.
DR GO; GO:0005871; C:kinesin complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin_1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
SQ SEQUENCE 459 AA; 51872 MW; 7C8487E9B7038E6A CRC64;

Query Match 44.2%; Score 744.5; DB 10; Length 459;
Best Local Similarity 56.5%; Pred. No. 1.3e-50;
Matches 161; Conservative 42; Mismatches 71; Indels 11; Gaps 5;

QY      49 DRVPHNETTKNVYEETIAAPIIDSALIOGNGTIFAYGQTASGKTYTMGSEDLGVIPRA 108
Db      45 DRFPEDCKTVQVYEARTKTEIVSAAVRGNGTIFAYGQTNSGKTHTRGSGPIEFGLPLA 104
QY      109 IHDIFQIKFPDRREFLLRVSMEIYNETITDLCGTQMKPLIIREDVNRNVYVADLTETEE 168
Db      105 VHDLDFTIYQDASREFLLRVSMEIYNEEDINDLL--APEHRKLOIHENLEKGIIVAGLRE 162
QY      169 EVVYTSEMALKWITKGEKSRHYGETKMNQSRSHITFRMILESEKGEPCNCEGSKVSHNLNLDLA 224
Db      163 EIVASPPQVLEMMFEGESHRIHGETNMNLYSSRSHITFRMILESEKGEPCNCEGSKVSHNLNLDLA 221
QY      225 VKYSHNLNLDLAGSRAAQTGAAGVRLKEGNCNINSLFLGQVIVKLSDG--QVGGFINVRDSDKSLRILQPAL 282

```

58 EIVSLFLFSFGVVFYVFFLLFADHVFDESNASTSVYELLTKDIIHAAVEGNGTAFAYGQTS 117
89 SKQTYTMMGSEDLGVIPRAIHDIQKIKKFPDRFLLRVSVMEIYNETITDLCCTQKM 148
118 SKQTYTMMGSEDLGVIPRAIHDIQKIKKFPDRFLLRVSVMEIYNETITDLCCTQKM 175
149 KPLIIRDNVNVVADITVEEVVYVSEMAKWIITKESRSHYGETONORSSRSHTIFRM 208
176 QRLQHEHLERGVFVAGLKEEIVSDAQILKIDSSEVNRHFGETNMVHSSRSHTIFRM 235
209 -----ILRESKEGPEPNCSEGVSVKSHLNLVDLAGSRAAQTGAAGVRLKEGCN 256
236 VRFPSYERDILLVIESR--GKNSSSDAIRVSVNLVLDLAGSRIAKTGAGGVRLQEGKY 293
257 INRSLPILQVVKIKLSDG-QVGGFINYRDSKLTIRLQNSLGGNPKTRITCTTPVS--FD 313
294 INKSLMILGNVINKUSDSKTLRAHPIYRDSKLTIRLQNSLGGNPKTRITCTTPVS--FD 353
314 ETLTALQFASAK 326
354 ESKGTQLQFASRAK 366

RESULT 7
Q869B8 PRELIMINARY; PRT; 1885 AA.
AC Q869B8
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Kinesin-related protein K4.
GN K4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OC NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98359834; PubMed=9693369;
RA de Hostos E.L., McCaffrey G., Sugang R., Pierce D.W., Vale R.D.;
RT "A developmentally regulated kinesin-related motor proteins from
Dictyostelium discoideum";
RL Mol. Biol. Cell 9:2093-2106 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Suyama E., Sutoh K.;
RT "Kinesin-related proteins from Dictyostelium";
Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB102780; BAC56912.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR001752; kinesin motor.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF00225; kinesin; 1.
DR Pfam; PF02370; M; 6.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
SQ SEQUENCE 1885 AA; 218216 MW; 15686AED3B007EC7 CRC64;

Query Match 42.6%; Score 719; DB 5; Length 1885;
Best Local Similarity 48.8%; Pred. No. 1e-47;
Matches 161; Conservative 56; Mismatches 101; Indels 12; Gaps 6;

QY 2 EGVAVCVVRPLNSREESLGETAQVYWKTDNNVI-YQVDSKSFNDRVPHGNETKN 60
DB ELNKIKVAIRVPLNSRE--LGIDQKIPWSISKDTISLQSNENINFTYDVGIDNTID 76
QY VVEETAAPTIDSAIQNGTIFAYGTASGKTYTMMGSEDLGVIPRAIHDIQKIKKFPDR 119
DB VYNAKSLVNSLNGTIFAYGTSSGKTFMRGTESIFGLIKLSIKDIFKSIDSI 136

222 VRVSVNLVLDLAGSRAAKTGAEGVRLKEGSHINKSLMTLGVVVKLSGVTQGHVPI 281
283 RDSKLTIRLQNSLGGNPKTRITCT--PVSPDETLTALQFASAK 325
282 RDSKLTIRLQNSLGGNPKTRITCT--PVSPDETLTALQFASAK 326

RESULT 6
Q91Q62 PRELIMINARY; PRT; 888 AA.
AC Q91Q62
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE T30E16.9
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,
RA Altarfi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Ruizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luross S.,
RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
RA Federspiel N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T30E16 from chromosome
I.";
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altarfi H., Bai B., Chin C., Chioi J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsy N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC009317; AAF9747.1; -.
DR PIR; D96619; D96619.
DR HSSP; P33176; 1BG2.
DR GO; GO:0005871; C:kinesin complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0007017; F:microtubule-based process; IEA.
DR InterPro; IPR001752; kinesin motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
SQ SEQUENCE 888 AA; 100694 MW; 0D640FBACEE0185 CRC64;

Query Match 43.8%; Score 738; DB 10; Length 888;
Best Local Similarity 46.4%; Pred. No. 1.1e-49;
Matches 173; Conservative 46; Mismatches 92; Indels 62; Gaps 8;

QY 6 VAVCVVRPLNSREESLGETAQVYWKTDNNVI-----Y 38
DB ICVAVVRP-----PAPENGASLWKVDNRLSLHKSLLDPTTTHSHAFVSGISISTDLI 57
QY QVDGSKSFN-----DRVFHGNFTKNVYEEIAPIIDSAIQNGTIFAYGTQTA 88

```

QY 120 PDRELLRVSYMEIYNETITLLCOT-QXMKPLIIRVDNRNVYVADLTETEEVYITSEMAI 178
Db 137 LEQDYLKVSYLEYNEIKOLLNPTISNKKKLIKIHEDYKGVVAVNLKEEIVISPDQIF 196
QY 179 KWTIGKSRHYGETKMNORSRSHITFRMILESKPEPSNCEGSKVSHNLVLDLAGS 238
Db 197 ALMNFGEERRHIGSTWMDSSRSHITFRMIOIQTCKQ-----NGTIQMSTLTVLDLAGS 251
QY 239 BRAAQGTGAAGVRLKEGNCINRSLFILGVIKKLSQGVGGFINVRDLSKLTILONSLGNN 298
Db 252 ERVSSTGAEGVRLKEGTHINKSLTSLKSLSEKTKQHQHVPRDLSKLTILQPSLGGN 311
QY 299 PKTRILITIPVSF-DETLTALOPASTAK 326
Db 312 SKTAILCTITPATTHQESISTLQFAKRAK 341

RESULT 8
O35059 PRELIMINARY; PRT; 160 AA.
AC O35059;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE Motor domain of KIF10 (Fragment).
GN CENPE OR KIF10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=97420736; PubMed=92751178;
RA Nakagawa T., Tanaka Y., Matsuoaka E., Kondo S., Okada Y., Noda Y.,
RA Kanai Y., Hirokawa N.;
RT "Identification and classification of 16 new kinesin superfamily (KIF)
RL proteins in mouse genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9654-9659 (1997).
DR EMBL; AB001426; BAA23386.1; -.
DR HSSP; P17119; 3KAR.
DR MGD; MGI:1098230; Cnpe.
DR GO; GO:0005871; C:kinesin complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
FT NON_TER 1
FT NON_TER 160
SQ SEQUENCE 160 AA; 18406 MW; 9E6E4F62642C241 CRC64;

Query Match
Best Local Similarity 41.9%; Score 707; DB 11; Length 160;
Matches 135; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 81 IFAYGQTASGTYTMMGSEDLGVIPRAIHDI FQIKKFPDPFLLRVSYMEIYNETITD 140
Db 1 IFAYGQTASGTYTMMGSEDLGVIPRAIHDI FQIKKFPDPFLLRVSYMEIYNETITD 60
QY 141 LLCTQKMKPLIIRVDNRNVYVADLTETEEVYITSEMAIKWTIKGKSRHYGETKMNORS 200
Db 61 LLCNAQMKPLIIRVDNRNVYVADLTETEEVYITSEMAIKWTIKGKSRHYGETKMNORS 120
QY 201 RSHITFRMILESRKGPSPNCEGSKVSHNLVLDLAGSE 239
Db 121 RSHITFRMILESRKGPSPNCEGSKVSHNLVLDLAGSE 159

```

```

RESULT 9
O3VK10 PRELIMINARY; PRT; 2013 AA.
AC O3VK10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cmet protein.
GN CMET OR CG6392.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.B., Gaig N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houstoun K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
DR EMBL; AE003631; AAF53088.2; -.
DR HSSP; P33176; 1BG2.
DR FlyBase; FBgn0040232; cmet.
DR GO; GO:0005699; C:kinetochore; IDA.
DR GO; GO:0007080; P:mitotic metaphase plate congression; IMP.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00150; SPEC; 3.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
SQ SEQUENCE 2013 AA; 231107 MW; 8A1A465581EF4F5F CRC64;

Query Match
Best Local Similarity 40.8%; Score 688; DB 5; Length 2013;
Pred. No. 3.3e-45;

```

Matches 162; Conservative 48; Mismatches 99; Indels 16; Gaps 8;
 QY 5 AVAVCVVRPLNRSRESLGETAQVYKWT--DNNVIYQVDG-SKSFNDRVFGHNETTKNY 62
 Db 8 SIQVCIKVRPCPGTSL-----WQVKERSIHLADSHAEFYVDFYVDEGASNOEYF 60
 QY 63 EETAAPIIDSAIQGNGTIFAYGQTASGKTYTMMGSEDLGLVPIRAIHDFOKIKKFPDR 122
 Db 61 DRMAKHIVHACMGFGNGTIFAYGQTSSGKTYTMMGDEQNPVGMVLAKEIFQOISSETER 120
 QY 123 EELLRVSYMEIYNETITDLLCGTQKWKPLIREDVNRNYYVADLTTEVVYTSSEM-ALKWI 181
 Db 121 DFLLRVGYEINYEKIYDILL--NKKQDLKIHSNGIYVNVN--CEECIITSEVDLLRL 176
 QY 182 TKGEKSRHYGETKMNQSRSHITFRMILSEKGEPSNCEGSKVSHNLNVLDSLGERA 241
 Db 177 CLGNKERTVGETNMNERSRSHAFKIIIESR-KSDHSD-DDAVIQSVNLNVLDSLGERA 234
 QY 242 AOTGAAGVRLKEGCNINRSILFQVVKIKLSDGVGFNYRDSKLTIRLQNSLGNPKT 301
 Db 235 DQTGARGARLKEGGHINKSLFLSNVKSLENADNRFNYRDSKLTIRLQASLGNNAFT 294
 QY 302 RIICITPVSFDETLTALQFASTAK 326
 Db 295 SIICITKPSIMESQSTLSFATRAK 319

RESULT 10

Q9NCGO PRELIMINARY; PRT; 2244 AA.
 ID Q9NCGO
 AC Q9NCGO;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Kinesin-like kinetochore motor protein CENP-meta.
 GN CMT OR C6392.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 EX MEDLINE=2031410; PubMed=10893249;
 RA Yucel J.K., Marszalek J.D., McIntosh J.R., Goldstein L.S.B.,
 RA Cleveland D.W., Philp A.V.;
 RT "CENP-meta, an Essential Kinetochore Kinesin Required for the
 RT Maintenance of Metaphase Chromosome Alignment in Drosophila.";
 RL J. Cell Biol. 150:11-12(2000).
 DR EMBL; AF220353; AAF32355.1; -.
 DR HSP; P33176; 1BG2.
 DR Flybase; FBgn040232; cmet.
 DR GO; GO:0005699; C:kinetochore; IDA.
 DR GO; GO:0007080; P:mitotic metaphase plate congression; IMP.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
 DR SEQUENCE 2244 AA; 257992 MW; FA6A3B2A541ADE0 CRC64;

Query Match 40.8%; Score 688; DB 5; Length 2244;
 Best Local Similarity 49.8%; Pred. No. 3.8e-45;
 Matches 162; Conservative 48; Mismatches 99; Indels 16; Gaps 8;
 QY 5 AVAVCVVRPLNRSRESLGETAQVYKWT--DNNVIYQVDG-SKSFNDRVFGHNETTKNY 62
 Db 8 SIQVCIKVRPCPGTSL-----WQVKERSIHLADSHAEFYVDFYVDEGASNOEYF 60
 QY 63 EETAAPIIDSAIQGNGTIFAYGQTASGKTYTMMGSEDLGLVPIRAIHDFOKIKKFPDR 122
 Db 61 DRMAKHIVHACMGFGNGTIFAYGQTSSGKTYTMMGDEQNPVGMVLAKEIFQOISSETER 120

QY 123 EELLRVSYMEIYNETITDLLCGTQKWKPLIREDVNRNYYVADLTTEVVYTSSEM-ALKWI 181
 Db 121 DFLLRVGYEINYEKIYDILL--NKKQDLKIHSNGIYVNVN--CEECIITSEVDLLRL 176
 QY 182 TKGEKSRHYGETKMNQSRSHITFRMILSEKGEPSNCEGSKVSHNLNVLDSLGERA 241
 Db 177 CLGNKERTVGETNMNERSRSHAFKIIIESR-KSDHSD-DDAVIQSVNLNVLDSLGERA 234
 QY 242 AOTGAAGVRLKEGCNINRSILFQVVKIKLSDGVGFNYRDSKLTIRLQNSLGNPKT 301
 Db 235 DQTGARGARLKEGGHINKSLFLSNVKSLENADNRFNYRDSKLTIRLQASLGNNAFT 294
 QY 302 RIICITPVSFDETLTALQFASTAK 326
 Db 295 SIICITKPSIMESQSTLSFATRAK 319

RESULT 11

Q8RW4 PRELIMINARY; PRT; 1055 AA.
 ID Q8RW4
 AC Q8RW4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative kinesin.
 GN AT4G39050.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Kaniya A., Karlin-Neumann G., Kawai J., Ishida J., Jones T.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RL "Arabidopsis Full Length cDNA Clones";
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY091060; AAM13881.1; -.
 DR GO; GO:0005871; C:kinesin complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0007017; F:microtubule-based process; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR InterPro; IPR001841; Znf ring.
 DR Pfam; PF00225; kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
 DR PROSITE; PS0089; ZF RING 2; 1.
 DR SEQUENCE 1055 AA; 116462 MW; BBF3709ACB40215B CRC64;

Query Match 40.5%; Score 683; DB 10; Length 1055;
 Best Local Similarity 47.6%; Pred. No. 3.3e-45;
 Matches 156; Conservative 55; Mismatches 107; Indels 10; Gaps 6;
 QY 1 ABEAVAVCVVRPLNRSRESLGETAQVYKWT--DNNVIYQVDGSKSFNDRVFGHNETTKN 60
 Db 94 SERDSISVTRFPEPLSDREYQVQDEAVAYPDGTLVRHYNPLTAYAFKDFGFGQATID 153
 QY 61 VYBEIAPIIDSAIQGNGTIFAYGQTASGKTYTMMGSEDLGLVPIRAIHDFOKIKKFP 120
 Db 154 YVDVAAPVVKAAAMEGVNGTVFAYGVTSSGKTYTMMGDEQNPVGMVLAKEIFQOISSETER 213
 QY 121 DRELLRVSYMEIYNETITDLLCGTQKWKPLIREDVNRNYYVADLTTEVVYTSSEMALKW 180

Best Local Similarity 39.8%; Pred. No. 1.8e-43;
Matches 159; Conservative 51; Mismatches 100; Indels 89; Gaps 10;

```
QY      6 VAVCVVRPLNREESLGETAQVYWKTDN--NVLYQVD----- 41
Db      237 VVVCVRMP--SRASSDSSEASV--WNCDSKKNRIFPTEHHPAIAKRTTSSERAGAGASIA 293

QY      42 -----GSKSFNFORVHGHNETTKNVYEEIAAPIIDSIAIQYNGTIFAYGQ 86
Db      294 AAPSSHDLDHEDPTSTYHFQDKLITGAQTDDMHSHIAPVVRAAVEGNGTVFAYGQ 353

QY      87 TASGKIYTMGSEDHLOVIPRAHDIFQIKKPPDRFILLRVSYMETINETITDLLCGTQ 146
Db      354 TSGSKTHMSGDAEPGVIPRAVEQIFQMIKDEPDRFILLRVSYLEYNETLKDLLA-- 410

QY      147 KMKPL-----IREDVNRNVYVADLTTEVV 171
Db      411 PLPLPAGTSGSSLTQTDTRPASPPIKGSSSHAAGSQSCTLRILEQKSSRVIIITGLREEIV 470

QY      172 YTSEMALKMITKGEKSRHYGETKMNQSRSSHTIFRMILESREKKEGPEPNCESGVKVSHLN 231
Db      471 TDANTVLCIQRQDERHVGATDWNERSRSRSHCVFOLTIESRSPASKE--VRISQLN 528

QY      232 LVDLAGSERAAGTGAAGVRLKEGCNINRSLFILGOVIKKLSGQVGG--FINYRDSKLTR 289
Db      529 LIDLASERAA---SQAERRKEGAFINKSLTLTGTVPVNGDAHIPYRDSKLTR 585

QY      290 ILQNSLGNPKTRIICTITPVS--FDETLTALOFATAK 326
Db      586 ILQTSLSGNARIAVICTLSFDPTEHANETLSTLAFGRCK 624
```

Search completed: July 29, 2004, 09:39:39
Job time : 14.9321 secs

Black sheet
vs P10